

ID	Score	Query		DB	ID	Description
		Match	Length			
1	694.2	61.9	2754	1	US-08-196-989B-1	Sequence 1, Appli
2	694.2	61.9	2754	1	US-08-760-936-1	Sequence 1, Appli
3	307	27.4	1137	3	US-09-082-088-1	Sequence 1, Appli
4	268	23.9	2232	1	US-08-196-989B-3	Sequence 3, Appli
5	268	23.9	2232	2	US-08-760-936-3	Sequence 3, Appli
6	195	17.4	1637	2	US-08-452-824-3	Sequence 3, Appli
7	187.6	16.7	1649	2	US-08-845-566-2	Sequence 2, Appli
8	139.8	12.5	2250	3	US-08-763-938-1	Sequence 1, Appli
9	138.2	12.6	1260	3	US-08-789-982-1	Sequence 1, Appli
10	130.2	11.6	1761	3	US-08-861-747-1	Sequence 1, Appli
11	130.2	11.6	1889	3	US-08-861-747-3	Sequence 3, Appli
12	125.4	11.2	1875	5	PCT-US96-1061B-1	Sequence 1, Appli
13	118.6	10.6	1065	4	US-09-325-897-1	Sequence 1, Appli
14	118.6	10.6	1356	3	US-09-927-803-13	Sequence 13, Appl
15	118.6	10.6	1523	3	US-08-997-803-12	Sequence 12, Appl
16	93.8	8.4	1338	2	US-08-044-812A-3	Sequence 3, Appli
17	93.8	8.4	1338	2	US-08-475-637-3	Sequence 3, Appli
18	93.8	8.4	1338	3	US-08-706-281A-11	Sequence 11, Appl
19	93.8	8.4	1338	4	US-09-191-359-3	Sequence 3, Appli
20	93.8	8.4	1338	4	US-09-097-231-11	Sequence 11, Appl
21	93.8	8.4	2185	2	US-08-467-948A-3	Sequence 3, Appli
22	93.8	8.4	2185	3	US-08-467-947A-3	Sequence 3, Appli
23	90	8.0	639	3	US-08-997-803-3	Sequence 3, Appli
24	89.4	8.0	1080	1	US-08-671-525B-5	Sequence 5, Appli
25	89.4	8.0	1080	1	US-08-672-109B-5	Sequence 5, Appli
26	89.4	8.0	1080	1	US-08-842-045-5	Sequence 5, Appli
27	89.4	8.0	1080	2	US-08-842-238-5	Sequence 5, Appli

	Query Match	61.9%	Score 694.2	DB 1	Length 2754
Best Local Similarity	82.2%				
Pred. No. 1.4e-145					
Matches 811	Conservative	0	Mismatches 173	Indels	3; Gaps 1


```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-082-088-1

```

Query Match 27.4%; Score 307; DB 3; Length 1137;
Best Local Similarity 61.0%; Pred. No. 3.8e-60;
Matches 520; Conservative 2; Mismatches 319; Indels 1

Qy	676	gtggccctgtacgtgcgcatactatgcgtgtgcgcgtcaagccacgcgtgacatggccgcc	735
Db	763	GTGGCCTTGTACGTCGGAATACTTCTAGTCGCTCAAGCCATCGAGACGTGCTGGT	822
Qy	736	ccgcagacgctagccctgtcctcaaacgcgtccaccatcgtctcagcgctctttatcgtctgc	795
Db	823	CCTCAGACGCTGGGCCCTGCTCAAGACAGTCACCATCTGACTGGGTGTTTTCATCATCTGC	882
Qy	796	tggctgcgcgccttcagcatcctcctcttgactatgcctgtcccgctccactctgcgcg	855
Db	883	TGGCTGCCGGCTTTTAGCATCCTTCTCTTAGACTACTCTGTCCGCTCGGGCCTGTCTCT	942
Qy	856	atcctctacaagcccaactactcttccgcgtctccaccctgaattccctgctctcaacccc	915
Db	943	GTCCTCTACAAAGGCCATTATTTCTTTGCCTTGGCCACCTCAACTCTGTCTCAACCT	1002
Qy	916	gtcattctacacgttggcgcagcgggacctgcgcggcgaggtgcttcggcgcgctgcagtc	975
Db	1003	GTCATCTATACATGGCGTAGCCGGACCTTCGGAGGGAGGTACTGAGGGCCCTGCTGTGC	1062
Qy	976	tggcgcgcgcgggttgggggtgcaggacgagggcggttcgggagcccgggccacacctc	1035
Db	1063	TGGGGCAGGGGAAGGGAGCACAGGGGGCA--GAGGTGGAAACCTGGTCACCGACTC	1119
Qy	1036	ctgcacatccgcagctccagctccctgcagaggggcgtgcacatgccacgctcacccacg	1095
Db	1120	CTGGCCCCCTCCGAGCTCCAGCTCCCTGGAGAGAGGCTTGCAATATGCTACATCGCCAACA	1179
Qy	1096	ttctcggaggggcaacacgcgtgctga	1122
Db	1180	TTTCTGGAGGGCAACACATGCTCTGA	1206

RESULTS

```

US-09-082-088-1
; Sequence 1, Application US/09082088
; Patent No. 6130067
; GENERAL INFORMATION:
; APPLICANT: TSUI, PING
; TITLE OF INVENTION: HUMAN EDG3sb GENE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: RATHER & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/082,088
; FILING DATE: 20-MAY-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GP-70453
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1137 base pairs
; TYPE: nucleic acid

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```
Sequence 3, Application US/08196989B
Patent No. 5585476
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/196,989B
FILING DATE: 15-FEB-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2232 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
NAME/KEY: CDS
LOCATION: 269..1420
US-08-196-989B-3

Query Match 23.9%; Score 268; DB 1; Length 2232;
Best Local Similarity 58.3%; Pred No. 2.4e-51;
Matches 508; Conservative 2; Mismatches 329; Indels 33; Gaps 1;

Qy 114 cttcatcgtatcctctgttgcgcacatgcagagacgaactcccgccaggtgacctcggc 173
Db || || || || || || || || || || || || || || || || || || || || ||
361 ctacacagcaagctgaacatcggagtcgagagagaccattgagcattaaactgacttcagt 420

174 cttcatcgtatcctctgttgcgcacatgcagagacgaactcccgccaggtgacctcggc 233
Db || || || || || || || || || || || || || || || || || || || || ||
421 ggtgtgtatcttcattctgtctgttgcattctctagagataatattgtcttgtaactat 480

Qy 234 gscggcaaacagcaagttccactcggaatgtacctgtttcttgggcaacctggccgctc 293
Db || || || || || || || || || || || || || || || || || || || || ||
481 ttggaaaacacacagattccaccggcccatgtactatttcataaggcaacctagccctctc 540

Qy 294 cgtatcactggcagcggtggttcgttagcccaatadttgctctctgttctgttcacgct 353
Db || || || || || || || || || || || || || || || || || || || || ||
541 ggacctgttagcaggagtggtctacacagctaacctgctgttctgtggggccaccacctta 600

Qy 354 gaggtcagcgtgtgagatgttttgcgggagggctctgctcctcactcaacgctctcggc 413
Db || || || || || || || || || || || || || || || || || || || || ||
601 caagctcacacctgcccacgtgtttctgcccgaaggaagtattgttggctctgtctgc 660

Qy 414 cttcttttcagcctccttgcctatgcattagccacagcggtggccattgccaagtcaa 473
Db || || || || || || || || || || || || || || || || || || || || ||
661 ctacgtcttcagccctctgttgcattgccttgccttgccttgccttgccttgccttgcct 720

Qy 474 gctgtatggcagcagcaagagctgcccgcattgctctgtcattcggggcctcgtggctcat 533
Db || || || || || || || || || || || || || || || || || || || || ||
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RESULT 5

```
US-08-760-936-3
Sequence 3, Application US/08760936
Patent No. 5856443
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/760,936
FILING DATE: December 6, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2232 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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; MOLECULE TYPE: DNA (genomic)
;
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 269..1420
US-08-760-936-3

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Query Match	23.9%	Score 268;	DB 2;	Length 2232;
Best Local Similarity	58.3%	Pred. No. 2.4e-51;		
Matches 508;	Conservative	2;	Mismatches 329;	Indels 33;
Gaps				
Qy 114	cttcacgtcatctctctgttgcccatgcaggagacgaactccgccaggtggcctcgccg	173		
Db 361	CTACACAGGCAAGCTGNACATCCGAGTGGAGAGGACCATGGCATTAACACTGACATCACT	420		
Qy 174	cttcatcgtcatctctctgttgcccatgttggtggaaaaacctctctgtgtcattcgtcgt	233		
Db 421	GGTGTTCATTCCTCATCTGCTGCTGATCATCTCTAGAGAAATATATTGTCTTGTAACAT	480		
Qy 234	gccccaaacagcaagttccactgcgaatgtacctgtttcttggtggcaacctggccgctc	293		
Db 481	TTGGAACACCAAGAAGTTCCACCGGCCATGTACTATTTTCATAGGCAACACTAGCCCTC	540		
Qy 294	cgatctactggcaggcgtgccctctgtagccaatadtgtctctctgtgclctgtcaacgt	353		
Db 541	GGACCTGTTAGTAGAGTGGCTTACACAGCTAACTGCTGTTGCTTGGGGCCACCACTA	600		
Qy 354	gaggctgacgcctgtgcagtgtgtttgccccggagggtctgtcctccatcacgtctctcgc	413		
Db 601	CAAGCTCACACCTGCCCAGTGGTTCTGCGGGAAGGAATGTTGTTGGCTCTGTCTCG	660		
Qy 414	ctctgtctcaagcctcctggccatgcgcattgagcgccacgtggccattgccaaggtcaa	473		
Db 661	CTCAGCTTCAGCCTCTGCTATTCGCAATGAGCGCTACATCACCATGCTGAAGATGA	720		
Qy 474	gctgtatggcaggaacaagagctgcgcagctctctgtcctcatcgggcctctcgtgctcat	533		
Db 721	ACTACACAAGGCGAGCAACAGCTCGCGCTCCTTCTGCTGATCAGTGCCTGCTGGTCA	780		
Qy 534	ctcgtggtcctcgttggtgccttgcctaccccttggctggaactgctggccacctcgaggc	593		
Db 781	CTCCCTCATCTCTGGTGGGCTGCCCATCATGGGTGGAACATGCATCAGCTCGCTGCCAG	840		
Qy 594	ctgtctcaactgtcctgcctctctacgcgaagcattatgtgtgctggtgacctatctt	653		
Db 841	CTGTCTCACCCGTGCTCCGCTCTACCAACAAGCACTATATTCTCTTGCACCACTGCT	900		
Qy 654	ctccatcatcctgttgcccatcgtggccctgtcagtgcgcattactcgtgtgtcgcctc	713		
Db 901	CACCTGCTCTGCTTTCCATPGTCATCCTCTACTGTCAGGATCTACTTCTTGTGTGAGGAC	960		
Qy 714	aagccagcgtgacatggcc-----gcccccgca	740		
Db 961	TCGAGCGCGCGCTGACCTCCGCAAGACATCTCCAGGCGAGCGGAGTTCCGAGAA	102		
Qy 741	gacgtagccctgtcctcaagcgttccaccatcgtgtcgtaggcgctttatcgtcgtcgt	800		
Db 1021	GTCCTGGCCCTGCTGAAGACAGTGATCTGCTCAGTGTCTTCACTTGCCTGCTGGGC	108		
Qy 801	gccgccttcgaatcctctcttgactatgcctgtcccgctccactcctgcccgcattcct	860		
Db 1081	CCCTCTCTTCATCTACTACTTTTAGATGTGGGTGCAAGGCGAAGACCTGTGCATPCCT	114		
Qy 861	ctacaagcccatcactttttcgcctctccacctgaattccctgtctcaaccccgctcat	920		
Db 1141	GTACAAAGCAGGTACTCTCTGGTGTCTGAACTCAGGTACCAACCAACCCATCAT	120		
Qy 921	ctacacgtggcgcagccggacctgcgcggg	952		
Db 1201	CTACACTCTGACCAATGAAGAGATGCGCCGGG	1232		

RESULT 6

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US-08-952-824-3
; Sequence 3, Application US/08852824C
; Patent No. 6060272
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: Human G-Protein Coupled Receptors
; FILE REFERENCE: 1488.1220000
; CURRENT APPLICATION NUMBER: US/08/852,824C
; CURRENT FILING DATE: 1997-05-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1637
; TYPE: DNA
; ORGANISM: genomic
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (50)..(1201)
; US-08-852-824-3

```

Query Match	17.4%	Score 195	DB 3	Length 1637	
Best Local Similarity	54.2%	Pred. No. 4.5e-35			
Matches 467	Conservative	2	Mismatches 374	Indels 18	Gaps 3
Qy	189	ctggtgcacattggtggaacacctctggtcctcatctgcgtgagccgcaaacacaa	248		
Db	217	cagctgcgtggtgctggagaaactgctggtgctggcgccatccacagccacatgcg	276		
Qy	249	gttcacctcgcaatgtacctgtttctgggcaacctggccctccgatctactcggcagg	308		
Db	277	gtcgcaacgcctggcttactattgcctggtgaacattacatgagtgaactgctcaggg	336		
Qy	309	cgtggcctctagcaataadthtgcctctcgtctcgtctcgtctcagctgagcgtcgt	368		
Db	337	cgcgctacactggcaacgtgctgctggggcgccgaccttcgctctggcgccgc	396		
Qy	369	cgagtggttgcccgagaggctctgcctccatcacgctctcgcctctgctctcagct	428		
Db	397	ccagtggctctcaggaaggcctgctctcacgcgcctggcgctccaccttcagct	456		
Qy	429	cttgcccatcgcatgtgagccacgtggccattg--ccaagttcaagctgtatggcag	485		
Db	457	gctctcactgcaggttgctcttgccaecatggtgcgcggtggcgagagcggggc	516		
Qy	486	cgacaagagctgcgcgatgctctcgtcatcagggcctcgtggctcactcgtcgtcct	545		
Db	517	caccaagaccagcgcgtactacggtctcagcctcgtggctgctggcgcgctgct	576		
Qy	546	cagtggtcgtgccatccttgctggaactgctggccactcagggcctgctcactgt	605		
Db	577	ggggatgctgcttgcctggcggtggaaactgctgtgccttggaccctgctccagct	636		
Qy	606	ctgctctctacgccaaagcattatgctgtgcgtggtgacacattcttcacatcct	665		
Db	637	ctcgccctactcgaagcctacatcctcttgcctggtgatcttcgcggcgtcct	696		
Qy	666	gttgcccatcgtggccctgtaogtgcgcgatctactcgtgtgtcgcgtcaagccagctga	725		
Db	697	ggccaccatcatgggctctatggggccatctccgcctggtgcagggcgagcgagaa	756		
Qy	726	cat-----ggcgcccgccgacagcactagcctgctcgaagcggctcacctgct	773		
Db	757	ggccccaagccagcgccggccgcgcaaggccgcgcctgctggaagcgggtgctgatgat	816		
Qy	774	gctaggcgtcttatcgtctgctgctgcgcgccttcagcatcctcctctctga---cta	830		
Db	817	ctcgtgcgtctcttggtgctgctggggaccactcttcggcgtgctgcgtgcgagctct	876		
Qy	831	tgctgtgcctgcctcactcgtgcccgatcctctcaaaagcccaactactttttgcgtctc	890		
Db	877	tgcttccaaacctctgggcccagagatcactcgtgggggcatggagctggtggtcctggccctggc	936		

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/763,938
 FILING DATE: 12-DEC-1996
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: JAHNS, Kristina M.
 REGISTRATION NUMBER: 41,092
 REFERENCE/DOCKET NUMBER: P8074-6018
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 638-5000
 TELEFAX: (202) 638-4810
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 2250 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 -08-763-938-1

Query Match 12.5%; Score 139.8; DB 3; Length 2250;
 Best Local Similarity 51.0%; Pred. No. 1.1e-22;
 Matches 326; Conservative 2; Mismatches 311; Indels 0; Gaps 0;

QY 136 gccatgcaggagacacctcccgccagggtggccttcacatcctctgttc 195
 DB 351 gccacagaaatgaacacacatgacgaagctggatggactggccatcactgttgcgtg 410
 QY 196 gccattgttggaacacctctctgtgctcattgcggtgcccgaacacagcaagtccac 255
 DB 411 ttcatcattgttgccacatctctggctggtggtggaatctacgtcaacggccgttccat 470
 QY 256 tcggcaatgaactgtttctgggaacctggccgctccgatctactgtggcagcggtggcc 315
 DB 471 ttccctattttattactgtggtggaacacctggctgctgcagacttcttgcgtggtggcc 530
 QY 316 ttcgtagcaaatdttgtctctgtgctgtgcaactgaggtgagcctgtgcagtg 375
 DB 531 tacttctactgtgttcaatacagagacctaataccggagactgactgtttagcacgtgg 590
 QY 376 ttgcccggagggtctgctccatcagcctctgctgctcctcttccagcctccctggcc 435
 DB 591 ctccctccggcaggccctctattgacaccgctgacagcttcttggccacactgtgct 650
 QY 436 atcgcaattgagccacgtggccattgccaaagtgcaagctgtatggcagcgaagagc 495
 DB 651 attgtctatcgagaggacacatcacgggtttccgcgatgcagctccatatacagcaatgagcaac 710
 QY 496 tgcgcgactcttctgctcactcggggcctcgtggctcactcgtgctcctcgtggtg 555
 DB 711 cggcggcgtggtggtgattgtgactatgactatggccattgtgattggtggtgtata 770
 QY 556 ccactcttggctggaactgctggccacctcagcctcagcctgctccactgctcctgcctc 615
 DB 771 ccagctgtggcgtggaaactgactctgtgatatcgatcactgttccacatggcaccctc 830
 QY 616 tacgcaagcattatgtgtgctggtggtgaccatctctccatcactcctgttggtgcaac 675
 DB 831 tacagtgactcctacttactgttctgggccatttttaaacctggtgacttttgggtcatg 890
 QY 676 gtgcccctgtacgtgcactcactcgtggtgctcgaagcagcagcgtgacatggccgcc 735
 DB 891 gtgggtctcttacccctcacatcttgggtgtggtgtggtgtggtgtggtgtggtgtggt 950
 QY 736 ccgcagacgttagcctgctcgaagcagcgttcaccatcgtg 774
 DB 951 catagtctggaccacagggaatcgggacaccatgatg 989

RESULT 9

US-08-789-982-1

; Sequence 1, Application US/08789982

Patent No. 6037146
 GENERAL INFORMATION:
 APPLICANT: Sathe, Ganesh
 APPLICANT: Bergsma, Derk
 TITLE OF INVENTION: CDNA CLONE HESCH90 THAT ENCODES
 TITLE OF INVENTION: A NOVEL 7- TRANSMEMBRANE RECEPTOR
 NUMBER OF SEQUENCES: 2
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SmithKline Beecham Corporation
 STREET: 709 Swedeland Road
 CITY: King of Prussia
 STATE: PA
 COUNTRY: USA
 ZIP: 19406
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FASTSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/789,982
 FILING DATE: 28-JAN-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER:
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Han, William T
 REGISTRATION NUMBER: 34,344
 REFERENCE/DOCKET NUMBER: ATGS00050
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 610-270-5219
 TELEFAX: 610-270-4026
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1260 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: cdna
 US-08-789-982-1

Query Match 12.3%; Score 138.2; DB 3; Length 1260;
 Best Local Similarity 50.6%; Pred. No. 2.1e-22;
 Matches 408; Conservative 2; Mismatches 367; Indels 30; Gaps 2;

QY 203 tgggtgaaacaccttctggtgctcattgcggtggccgaaacagcaagttccactcgca 262
 DB 272 TGCTGACCAATCTGCTGGTCATAGCAGCCATCGCTCCACACGGCGCTTCACACGCGCA 331
 QY 263 tgtaacctgtttctgggcaacctggcgcctccgatctactggcagcgctggccttcgtag 322
 DB 332 TCTACTACCTGCTCGCAATCTGCGCGGCTGACCTCTCGCGGGCTGGGCTACCTCT 391
 QY 323 ccaatadttgctctctggtcctctcaagctgaggtgagcctgtgagtggtttgcc 382
 DB 392 TCCATCATGTCACACTGCTCCCGCACACGCCGACTTTCACCTTAGAGGCTGGTTCCTGC 451
 QY 383 gggagggtctctcctccateacgctctcgctctgtcttcagcctcctggccatcgcca 442
 DB 452 GGCAGGGCTTCTGGACACAAAGCTCACTGCTGGTGGCCACACTGCTGGCCATCGCGG 511
 QY 443 ttgagcgcacgtggccattgccaaaggtcaagctgtatggcagcgacagaagctgccga 502
 DB 512 TGGAGCGCACCCGAGTGTGATGGCCGTGACGTGCACACGGCGCTGCCCGTGGCGCG 571
 QY 503 tgcctctgctcactcggggcctcgtggtcactcgtggtcactcgtggtggtggtgccatcc 562
 DB 572 TGGTCATGCTCATTTGTGGGCGGTGTGGGTGGCTGCCCTGGGCGTGGCTGGCTGCC 631
 QY 563 ttgctggaactgctggggccacctcaggtgctgctccactgtcctcctcactacgcca 622


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; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Human
; US-09-325-897-1

      10.6%; Score 118.6; DB 4; Length 1065;
      Best Local Similarity 52.1%; Pred. NO. 4.8e-18;
      Matches 261; Conservative 2; Mismatches 238; Indels 0; Gaps 0;

QY 199 attgtggtggaagaacctttctgtgtctcattgcggtgcccgcgaacacagcaagtctccactcg 258
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Db 130 attttttttctaatctctgtgtcatcgcgcgagtcatcaaaacagaaaatttcatttc 189
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QY 259 gcaatgtacctgtttctgvgcaacctggccctccgactctactgagcggtggccttc 318
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Db 190 cccctctactaccctgttgtaatttagctgctgccgattcttcctgctgaatgcctat 249
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QY 319 gtagccaataddttgtctctctgtgctctgtcacgtgaggtgacgcctgtgcagtggttt 378
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Db 250 gtattctgatgtttaacacagcccagtttcaaaaactttgactgtcaaccgctggtt 309
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QY 379 gcccgggagggtctgctctccatcaacgctctcgccctctgtcttcagcctctggccatc 438
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Db 310 ctccgtcaggggctctggacagttagctgttgactgtctccctcaccaactgctggtttac 369
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QY 559 atcttgctgggaactgcctgggcccaactcagggcctgctccactgctcgtcctctctac 618
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Db 490 acactggctgggaattgacctctcgaacatctcgtctgctctccttccctggccccattac 549
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: CURRENT APPLICATION DATA:
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: APPLICATION NUMBER: US/08/997,803
: FILING DATE: 24-DEC-1997
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Wong, King L.
:
: REGISTRATION NUMBER: 37,500
: REFERENCE/DOCKET NUMBER: P8074-7020
:
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 638-5000
: TELEFAX: (202) 638-4810
: INFORMATION FOR SEQ. ID NO. 13:
:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1356 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: DNA
: -08-997-803-13
:

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Query Match	10.6%	Score 118.6	DB 3	Length 1356
Best Local Similarity	52.1%	Pred. No. 5	le-18	
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OY	199	attgtgtggaacacctctgtgtgtctcattgcgtgtgcccgaacacagaagttccactcg	258	
Db	165	ATTTTTTTCTTAATCTCTGGTCATCGCGGCAGTGATCAAAACACAGAAATTCATTTC	224	
OY	259	gaatgtacctgttcttgggcaaccttggccgtccgatctactggcagcgctggcccttc	318	
Db	225	CCCTTTTACTACCTGTGTGGCTAATTTAGCTGTCTGCCGATTTCTCGGTGGAAATTCCTAT	284	
OY	319	giagcaaatdtdtctctctgtgctctgtcaocgtgaggtgacgcctgtgcagtggttt	378	
Db	285	GTATTCCTGATGTTAAACACAGCCCGAGTTTCAAAAACCTTTGACTGTCAACCGCTGGTTT	344	
OY	379	gccctggagggctctgcctccatcacgctctgcgcctctgcctgcctctgcctgcgcctc	438	
Db	345	CTCCGTGACGGGCTTCTGACAGTAGCTGTGACTGTCTCCCTCACCAACTTGTCTGGTTATC	404	
OY	439	gcattgagcgcaactgtgccattgccaaggtcaactgtatggcagcgacagaagctgc	498	
Db	405	GCCGTGGAGAGGCACATGTCAATCATGAGATGCGGGTCCATAGCAACCTTGACCAAAAG	464	
OY	499	cgcatgctctctgcctcagggcctcgtggctcactcgtcgtcctcgtcgtcgtcgtcgc	558	
OY	465	AGGGTGACACTGCTCATTTTGTCTGTCTGGGCCATCGCCATTTTATGGGGGGGGTCCC	524	
OY	559	atccttggctgaaactgctggggccacctcagggcctgtcctcactgtcctgcctctctac	618	
Db	525	ACACTGGGTGGAATTCGCTCTGCAACATCTCTGCCTGTCTTCCCTGGCCCCCATTTTAC	584	
OY	619	gccaaagcattatgtcctgtgctgtgtgacattcttctccatcctcgttggccactgtg	678	
Db	585	AGCAGGAGTTACCTTGTTTTCTGGACAGTGTCCAACCTCATGGCCCTTCCTCATCATGGTT	644	
OY	679	gccctgtacgtgcgatctac	699	
Db	645	GTGGTGTACCTCGGGATCTAC	665	

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RESULT 15
US-08-997-803-12
; Sequence 12, Application US/08997803
; Patent No. 6057126
;
; GENERAL INFORMATION:
; APPLICANT: CHUN, Jerold J.M.
; APPLICANT: GUPTA, Ashwani
; APPLICANT: MUNROE, Donald G.
; APPLICANT: VYAS, Tejal B.
;
; TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
; NUMBER OF SEQUENCES: 15

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaïdo, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street, N.W., Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-5701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997.803
FILING DATE: 24-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wong, King L.
REGISTRATION NUMBER: 37,500
REFERENCE/DOCKET NUMBER: P8074-7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 261..1322
US-08-997-803-12

	Query Match	10.6%	Score 118.6	DB 3	Length 1523	
	Best Local Similarity	52.1%	pred. No. 5.2e-18			
	Matches 261	Conservative 2	Mismatches 238	Indels 0	Gaps 0	
QY	199 attgtgtggaacacctctgtgtcattgcgtggtgcccgaacagcaagtctccactcg	258				
Db	390 ATTTTCTTCTAAATCTGTGTCATCGCGCAGTGTCAAAAACAGAAAAATTTCAATTC	449				
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Db	450 CCCTTTTACTACCTGTGGCTAATTAGTCTGCCGATTTCTTCGTGGAAATTCGCTAT	509				
QY	319 gtaccgaatadttgctctctggctctgtcaagctgaggctgagcgctgtgcaatgattt	378				
Db	510 GTATCTCTGATGTTTAACACAGGCCAGTTTCAAAAACCTTTGACTGTCAACCGCTGGTTT	569				
QY	379 gccgggaggcctgctccatcaacgctctcgccctctgtcttcagcctctctggccatc	438				
Db	570 CTCGCTCAGGGGCTTCTGGACAGTAGCTTGACTGTCTCCCTCACCACCTTGTCTGGTTATC	629				
QY	439 gccattgagcgcacatggtccattgccaaaggtcaagctgtatggcagcagcaagagctgc	498				
Db	630 GCCGTGGAGGACACATGTCAATATGAGGATCGGGGTCCATAGCAACCTTGACCAAAAAG	689				
QY	499 cgcattctctgtctatcggggctcgtgtgctcatctcgtgtccctcgtggcctgcc	558				
Db	690 AGGGTGACACTGCTCATTTTGTCTTGGGCCATCGCCATTTTATGGGGGGCGTGCCCC	749				
QY	559 atccttggctggaactgcctgggccacctgagcgctgtccactgtccctgcctctctac	618				
Db	750 ACACCTGGGTGGAATTCGCTCTGCAACATCTCGCGCTGCTCTTCCCTGGGCCCCATTTAC	809				
QY	619 gccaaacattatgtcgtgctggtggaaccattcttccatcatcctgttggccatcgtg	678				
Db	810 AGCAGAGATACCTTGTTTCTGGACAGTGTCCAAGCTCATGGCTTCCTCATCATGGTT	859				
QY	679 gccctgtacgtgcgcacatctac	699				

Db 870 GTGGTGTA CCTGCGGATCTAC 890

Search completed: December 20, 2001, 10:06:16
Job time: 3055 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 20, 2001, 10:06:41 : Search time 2907.25 seconds
(without alignments)
6366.785 Million cell updates/sec

Title: US-09-274-752d-4
Perfect score: 1122
Sequence: 1 atgggcagctgtactcgga.....agggcacacggtggtctga 1122

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Summary: 1472140 seqs, 8248589755 residues
Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.ov.*
- 5: gb.pat.*
- 6: gb.un.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
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- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.om.*
- 20: em.or.*
- 21: em.ov.*
- 22: em.pat.*
- 23: em.ph.*
- 24: em.pl.*
- 25: em.ro.*
- 26: em.sts.*
- 27: em.sy.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htgo.hum.*
- 31: em.htgo.inv.*
- 32: em.htgo.hum.*
- 33: em.htg.hum.*
- 34: em.htg.inv.*
- 35: em.htg.rod.*
- 36: em.htg.other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Result No.	Score	Match	Length	DB	ID	Description
1	988.8	88.1	1062	9	AF034780	AF034780 Homo sapi
2	984	87.7	156503	9	AC011511	AC011511 Homo sapi
3	710.2	63.3	1059	10	AF108020	AF108020 Mus muscu
4	708.6	63.2	214006	2	AC073775	AC073775 Mus muscu
5	708.6	63.2	220103	2	AC073781	AC073781 Mus muscu
6	697.4	62.2	1139	6	E07989	E07989 DNA encodin
7	697.4	62.2	1139	10	AB016931	AB016931 Rattus no
8	694.2	61.9	1059	6	AX085544	AX085544 Sequence
9	694.2	61.9	2754	6	AR027718	AR027718 Sequence
10	694.2	61.9	2754	6	I32244	I32244 Sequence 1
11	694.2	61.9	2754	10	RNU10699	U10699 Rattus norv
12	691.2	61.6	1056	10	AF022138	AF022138 Rattus no
13	470.6	41.9	607	10	AF289992	AF289992 Cavia por
14	402.4	35.9	573	10	AF090995	AF090995 Rattus no
15	387	34.5	540	10	MUSGPR13	L20334 Mouse EDG-1
16	383.6	34.2	1110	5	AF260256	AF260256 Danio rer
17	320.2	28.5	977	4	AY011726	AY011726 Artibeus
18	314.2	28.0	978	10	AY011714	AY011714 Myocastor
19	313.4	27.9	978	10	AY011704	AY011704 Muscardin
20	309	27.5	978	4	AY011694	AY011694 Sorex ara
21	308.6	27.5	1134	9	AF022139	AF022139 Homo sapi
22	308.6	27.5	1137	6	AX085542	AX085542 Sequence
23	308.6	27.5	2327	9	HSEB3	X83864 H.sapiens E
24	307	27.4	1137	6	AR112475	AR112475 Sequence
25	300.6	26.8	978	10	AY011708	AY011708 Hystrix b
26	297.8	26.5	978	4	AY011737	AY011737 Tapirus i
27	296.4	26.4	978	4	AY011717	AY011717 Ochotona
28	296.2	26.4	978	9	AY011720	AY011720 Lemur cat
29	294.2	26.2	975	4	AY011739	AY011739 Leopardus
30	293.2	26.1	978	4	AY011697	AY011697 Procavia
31	292.6	26.1	975	4	AY011738	AY011738 Fells cat
32	292.6	26.1	975	4	AY011740	AY011740 Panthera
33	292.6	26.1	978	4	AY011690	AY011690 Tamandua
34	291.6	26.0	978	4	AY011719	AY011719 Tupia mi
35	291.4	26.0	978	4	AY011691	AY011691 Myrmecoph
36	291.4	26.0	978	4	AY011736	AY011736 Ceratophe
37	291.4	26.0	978	9	AY011718	AY011718 Cynoceph
38	291	25.9	978	4	AY011735	AY011735 Equus cab
39	291	25.9	1695	5	AF164114	AF164114 Fugu rubr
40	289.8	25.8	978	4	AY011687	AY011687 Choloepus
41	289.4	25.8	978	10	AY011711	AY011711 Heterocep
42	288.4	25.7	978	10	AY011709	AY011709 Erethizon
43	287.2	25.6	978	4	AY011728	AY011728 Roussetus
44	286.2	25.5	978	4	AY011734	AY011734 Okapia jo
45	286.2	25.5	978	10	AY011715	AY011715 Agouti ta

ALIGNMENTS

RESULT	1					
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LOCUS	AF034780	1062 bp	mRNA	PRI	01-JAN-1999	
DEFINITION	Homo sapiens	lysophospholipid	receptor	Edg5	mrna, complete cds.	
ACCESSION	AF034780					
VERSION	AF034780.1	GI:4090955				
KEYWORDS						
SOURCE	human.					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	1 (bases 1 to 1062)					
AUTHORS	MacLennan,A.J., Browe,C.S., Gaskin,A.A., Lado,D.C. and Shaw,G.					
TITLE	Cloning and characterization of a putative G-protein coupled					
	receptor potentially involved in development					
JOURNAL	Mol. Cell. Neurosci. 5 (3), 201-209 (1994)					
MEDLINE	94373324					
REFERENCE	2 (bases 1 to 1062)					
AUTHORS	An,S.					
TITLE	Edg5, a Human homolog of rat H218 that is a functional receptor for					

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lysophingolipids
Unpublished
REFERENCE 3 (bases 1 to 1062)
AUTHORS An,S.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-1997) Medicine, UC-San Francisco, 533 Parnassus
Ave., San Francisco, CA 94143-0711, USA
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CAIVFENGLVLAIVARNKSFHSAFYLFLGNLAASDLGAVFAVANTLLSGSVFLRLTP
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VLGGPILGNLGLHLEAGSTVLPYAKHVKVIVTIFSIILAIYVALIVRICVYVRS
SHADMAAPOTALLKTVITVLGVFIVCWLPAPFSLILLDYACPVHSPILYKAHYFAV
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ERGMHPTSPTELENTVV"
BASE COUNT 166 a 367 c 294 g 235 t
ORIGIN

Query Match 88.1%; Score 988.8; DB 9; Length 1062;
Best Local Similarity 94.5%; Pred. No. 6.4e-162;
Matches 1060; Conservative 0; Mismatches 2; Indels 60; Gaps 1;

QY 1 atgggcagctgttactcggagtagctgaaccccaacaaaggtccaggaaactataattat 60
DB 1 ATGGGCAGCTGTGACTCGGAGTAGCTGAACCCCAACAAAGGTCCAGGAACACTATAATTAT 60

QY 61 accaagagacgtgaaacgacgaggagacacactcccgccaggtggcctcgcccttcac 120
DB 61 ACCAAGAGACGCTGGAAC-----80

QY 121 gtcactcctgttgcccatcaggagacacactcccgccaggtggcctcgcccttcac 180
DB 81 -----GCAGGAGACGACCTCCGCCAGGTGGCTCGGCTTCATC 120

QY 181 gtcactcctgttgcccatcgttggtggaacactcttctgtctcattgctgggcccga 240
DB 121 GTCATCTCTGTGCGCCATGTGTTGGTGAACACTTCTGTGCTCATTTGGTGGCCCGA 180

QY 241 aacagcaagttccactcggcaatgtacctttcttggaacactgcccgcctccgacta 300
DB 181 AACAGCAAGTTCCACTCGGCAATGTACTGTTTCTGGGCAACCTGGCCGCTCCGATCTA 240

QY 301 ctggcagggtggtcctctagcaaataddttgctctctggtctgtctcagctgaggtg 360
DB 241 CTGGCAGGCTGCGCTTCGTAGCAATACCTTGTCTCTGCTGTCTGTCACGCTGAGGCTG 300

QY 361 agcctgtgagtggttggccggagggtctgctcctcaatcagctctcggcctctgtc 420
DB 301 ACOCCTGTGAGTGGTGTGCGGGAGGGCTCTGCCTCCATCATCGCTCTCGGCTCTGTC 360

QY 421 ttacgctcctgcccacgtcattgagccacgtggtggtccattccaaaggtcaagctat 480
DB 361 TTACGCTCTCTGCGCATGCGCATGTGAGCGCACGTGCGCATTCGCAAGGTCAAGCTGTAT 420

QY 481 ggcagcaagaagctgcccagctgtctctcctcagctgggcccctcgtggtcactcgtg 540
DB 421 GGCAGGCAAGAAGCTGCGCATGCTCTCTCTCATCGGGCCCTCGTGGCTCATCTCGCTG 480

QY 541 gtcctcgttggtcctgcccactccttggctggaactgctgggcccacactcaggcctctcc 600
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RESULT 2
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LOCUS Homo sapiens chromosome 19 clone CTD-2369P2, complete sequence.
AC011511
VERSION AC011511.10 GI:15187226
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 156503)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 156503)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 156503)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE Direct Submission
JOURNAL Submitted (15-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT On Aug 15, 2001 this sequence version replaced gi:14971180.
Draft Sequence Produced by DOE Joint Genome Institute
www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.
STS Content:
WI-14289 G22683
WI-7031 G06361.
Location/Qualifiers
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Best Local Similarity	94.2%;	Pred. No. 1.1e-161;		
Matches 1057;	Conservative	0;	Mismatches	5;
			Indels	60;
			Gaps	1;

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Query Match      63.3%; Score 710.2; DB 10; Length 1059;
Best Local Similarity 83.2%; Pred. No. 1.1e-113;
Matches 821; Conservative 0; Mismatches 163; Indels 3; Gaps 1;
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Db	136	GCCATCGTGGAGAACTCTTGCTGTCTATTGTCAGTGGCCAGGACAGCAAGTTCCAC	195
Qy	256	tcggcaaatgaactgtttctgtgggaacactggccgctccgatactactatgtggaaggcgtgccc	315
Db	196	TCAGCAATGTACTGTTCTTCCTGGCAACCTGGCAGCTCTGACCTGCTTGGCAGGGCTGGCC	255
Qy	316	ttcgtagcaaataddttgctctctgtgctctgtcaacgttgaggcttgacgacctgtgcagtgg	375
Db	256	TTGCTGGCCACACCTTACTCTCAGGGCATGTCACTCTGCTTAACTCCGCTCAGTGG	315
Qy	376	tttgccgggagggtctgtcctccatcaacgtctctcgtgacctgtgttcttaagcctcttgccc	435
Db	316	TTTGGCCGAGAGGTCTCCGCCCTTCATCAGCTCTCCGCTCGGCTCTTATAGCTCTCTGGCC	375
Qy	436	atcgcccatlgagcgcaactggccattgccaaaggtccaagctgtatggcagcgacaagc	495
Db	376	ATGCGCCATCGAGAGACAAGTGGCCCTCGCCAAAGGTCAAGCTCTACGGCAGTGACAAAAGC	435
Qy	496	tgccgcatgtcttctgtcctacatcggggacctcgttggtcctatctcgtggtcctcgttgacctg	555
Db	436	TGCGGAATGCTGATGCTCATCGGGGCTCTTGGCTGATATCGCTGATTCTGGTGGGCTTG	495
Qy	556	ccatccttggtggaactgctggggccacctcgaggcctgctccactgctcctcctctc	615
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Qy	616	taaggcaagcattatgtgtctgtcggtgtgacattcttccatcactcctgttggccatc	675
Db	556	TATGCTAAGCACTACGTGCTCTCGTGGTGCACCATCTTCTCGTCACTTACTTGGCTATC	615
Qy	676	gtggccctgtacgtgcgcactactactgtgtgtgtccgtccaaagcactgacatggccgc	735
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Qy	736	cgcgacagctagcctcgtcgaagcgtgcacactcgtcgtcgtcgtcgtcttatcgtctgc	795
Db	676	CCTCAGACGCTAGCCCTGCTCAAGACGCTCACCATCGTACTGGGTGTTTTCATCATCTGC	735
Qy	796	tggctgcgcgccttcgaactcctcctcttgagatgtgctgtccogtccactcctcgcgc	855
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Qy	856	atcctctcaaaagccactaacttttccgctctccacctgaattccctcgtcaacccc	915
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Qy	916	gtcatatacactggtgcagccgggacctggcggggaggtgcttcgycgctgcagtgc	975
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Qy	976	tggcgccgggggtgggggtgcaaggacggaggcgggtcgggaccccgggccacacctc	1035
Db	916	TGGCGGAGAAGGAAGAGGTGACGGGAGCGCA---GAGGTGGGAACCCCTGGTCCACCGACT	972
Qy	1036	ctgccactccgagctccagctcccttgagaggggcatgacatgcccacgtccaccacg	1095
Db	973	CTGCCCTCCGAGCTCCAGCTCCCTGGAGAGAGCATGCATATGCTATACATCACCGACA	1032
Qy	1096	ttcttgaggggcaacacggtggtctga	1122
Db	1033	TTTCTGGAGGTTAACACAGTGTCTGA	1059

WILLIAM

RESULT
AC073775

AC073775	LOCUS	214006 bp	DNA

HTC

AC073775 214006 bp DNA HTG 18-JUL-2000
Mus musculus clone RP23-382B11, WORKING DRAFT SEQUENCE, 9 ordered
pieces.

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AC073775
AC073775.2 GI:9256790
HTG: HTGS_PHASE2; HTGS_DRAFT.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 214006)
DOE Joint Genome Institute.
Sequencing of Mouse
Unpublished
2 (bases 1 to 214006)
DOE Joint Genome Institute.
Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810392.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov

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Project Information
Center Project Name: 1883595
Center clone name: RPCI-23_382B11
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Summary Statistics
Consensus quality: 209197 bases at least Q40
Consensus quality: 212478 bases at least Q30
Consensus quality: 212996 bases at least Q20
Estimated insert size: 218930; agarose-fp estimation
Estimated insert size: 213656; sum-of-contigs estimation
Quality coverage: 9.1 in Q20 bases; agarose-fp estimation
Quality coverage: 9.33 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1
11489: contig of 11489 bp in length
11589: gap of unknown length
11590: 72347: contig of 60758 bp in length
72348: 72447: gap of unknown length
72448: 79269: contig of 6822 bp in length
79270: 79369: gap of unknown length
79370: 79945: contig of 576 bp in length
79946: 80045: gap of unknown length
80046: 101339: contig of 21294 bp in length
101340: 101439: gap of unknown length
101440: 118105: contig of 16666 bp in length
118106: 118205: gap of unknown length
118206: 142604: contig of 24399 bp in length
142605: 142704: gap of unknown length
142705: 151311: contig of 8607 bp in length
151312: 151411: gap of unknown length
151412: 214006: contig of 62595 bp in length.
Location/Qualifiers
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/db_xref="taxon:10090"
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/clone.lib="RPCI mouse BAC library 23"
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BASE COUNT
ORIGIN

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Query Match
Best Local
Matches 82

63.2%; Score 708.6; DB 2; Length 214006;
83.1%; Pred. No. 4.8e-114;
tive 0; Mismatches 164; Indels 3; Gaps 1;

	DEFINITION	Mus musculus clone RP23-398A12, WORKING DRAFT SEQUENCE, 13 ordered pieces.
	ACCESSION	AC073781
	VERSION	AC073781.2 GI:9964815
	KEYWORDS	HTG; HTGS_PHASE2; HTGS_DRAFT.
	SOURCE	house mouse.
	ORGANISM	Mus musculus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
	REFERENCE	1 (bases 1 to 220103) DOE Joint Genome Institute. Sequencing of Mouse Unpublished
	AUTHORS	2 (bases 1 to 220103) DOE Joint Genome Institute. Direct Submission
	TITLE	Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
	JOURNAL	On Sep 2, 2000 this sequence version replaced gi:8810398.
	COMMENT	-----Genome Center Center: Joint Genome Institute Center Code: JGI Web site: http://www.jgi.doe.gov ----- Project Information Center Project Name: 1889716 Center clone name: RPCI-23_398A12 ----- Summary Statistics Consensus quality: 209550 bases at least Q40 Consensus quality: 216439 bases at least Q30 Consensus quality: 217881 bases at least Q20 Estimated insert size: 229553; agarose-fp estimation Quality coverage: 6.87 in Q20 bases; agarose-fp estimation Quality coverage: 6.98 in Q20 bases; sum-of-contigs estimation. NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter. This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved. 1 40803: contig of 40803 bp in length 40904 40903: gap of unknown length 40904 41523: contig of 620 bp in length 41524 41623: gap of unknown length 41624 55711: contig of 14088 bp in length 55712 55811: gap of unknown length 55812 61812: contig of 6001 bp in length 61813 61912: gap of unknown length 61913 117606: contig of 55694 bp in length 117607 117706: gap of unknown length 117707 122273: contig of 4567 bp in length 122274 122373: gap of unknown length 122374 123402: contig of 1029 bp in length 123403 123502: gap of unknown length 123503 124793: contig of 1291 bp in length 124794 124893: gap of unknown length 124894 127965: contig of 3072 bp in length 127966 128065: gap of unknown length 128066 150779: contig of 22714 bp in length 150780 150879: gap of unknown length 150880 170652: contig of 19773 bp in length 170653 170752: gap of unknown length 170753 213515: contig of 42763 bp in length 213516 213615: gap of unknown length 213616 220103: contig of 6488 bp in length.
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RESULT	6
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LOCUS	1139 bp RNA PAT 29-SEP-1997
DEFINITION	DNA encoding a peptide that has receptor activity coupling with GTP-binding protein.
ACCESSION	E07989
VERSION	E07989.1 GI:2176120
KEYWORDS	JP 1994234797-A/1.
SOURCE	Homo sapiens
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
AUTHORS	Takuwa,A.
TITLE	NEW PEPTIDE HAVING RECEPTOR ACTIVITY AND DNA ENCODING THE PEPTIDE
JOURNAL	Patent: JP 1994234797-A 1 23-AUG-1994;
COMMENT	TSUMURA & CO, TAKUWA AKIRA OS Homo sapiens (human) PN JP 1994234797-A/1 PD 23-AUG-1994 PF 10-FEB-1993 JP 1993044330 PI TAKUWA AKIRA PC C07K13/00,C07H21/04,C12N15/12,C12P21/02; CC strandedness: Double; CC topology: Linear; FH key Location/Qualifiers EH source 1..1139 /organism='Homo sapiens' FT CDS 37..1095 /product='a peptide that has receptor activity with GTP-binding protein'. FT FT Location/Qualifiers FT 1..1139 /organism="Homo sapiens" BASE COUNT 210 a 359 c 295 g 275 t ORIGIN
Query Match	62.2%; Score 697.4; DB 6; Length 1139;
Best Local Similarity	82.4%; Pred. No. 1.8e-111;
Matches 813; Conservative	0; Mismatches 171; Indels 3; Gaps 1;
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Qy 256 tcggcaatgatccttgtttctgvgaaacctggccctccgactcactgcagcgctgacc 315	
Db 232 TCAGCCATGTACCTGTTTCCTCGGCNAACCTGGCAGCCTCCGACCTGCTGGCAGGCGTGCC 291	
Qy 316 ttctagccaatatdttgctctctctgtctgtcacgctgagcgtgacgctctgtcagtg 375	
Db 292 TTCGTGGCCAACAACCTTGCTCTCCGGACCTGTCAACCTGTCAACCTCCCTTGCAGTGG 351	
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SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2754)
AUTHORS MacLennan, A. John.
TITLE Molecular cloning and expression of G-protein coupled receptors
JOURNAL Patent: US 5856443-A 1 05-JAN-1999;
FEATURES Location/Qualifiers
Source
BASE COUNT 569 a 794 c 714 g 677 t
ORIGIN
Query Match 61.9%; Score 694.2; DB 6; Length 2754;
Best Local Similarity 82.2%; Pred. No. 5.1e-111;
Matches 811; Conservative 0; Mismatches 173; Indels 3; Gaps 1;
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Qy 196 gccattgtgtggaacacctctctgtctcattgcggtggtggccgaaacagcaagttccac 255
Db 283 GCCATCGTGGTGGACACCTTCTGTGTCTATCGCAGTGGCCAGGAAACAGCAAGTTCAC 342
Qy 256 tcggcaatgtacctgtttctgggcaacctggcgcctccgactcactgacagcaggtccac 315
Db 343 TCAGCCATGTACCTTCTCGGCAACCTGGCAGCTCGGACCTGCTGGCAGGCGTGGCC 402
Qy 316 ttctgagcaataaddttgtctctgtcctcctcctcctcctcctcctcctcctcctc 375
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Db 523 ATTGCCATCGAGAGCAAGTGGCCATCGGCAAGGTCAAGGTCAAGGTCAAGGTCAAGG 582
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Qy 616 tacgcaagcattatgtctgtggtggtggtggtggtggtggtggtggtggtggtggtg 675
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Db 1120 CTGCCCTCCGCAAGTTCAGCTCCCTGGAGAGAGCTTGCATATGCTTACATCGCAACA 1179
Qy 1096 ttctgaggggcaacacggtggtctga 1122
Db 1180 TTCTGGAGGGCAACACAGTGTGTCTGA 1206
RESULT 10
I32244
LOCUS I32244 2754 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5585476.
ACCESSION I32244
VERSION I32244.1 GI:1823035
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2754)
AUTHORS MacLennan, A. J.
TITLE Molecular cloning and expression of G-protein coupled receptors
JOURNAL Patent: US 5585476-A 1 17-DEC-1996;
FEATURES Location/Qualifiers
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BASE COUNT 569 a 794 c 714 g 677 t
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Best Local Similarity 82.2%; Pred. No. 5.1e-111;
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Job time: 3227 sec

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Date: Dec 20, 2001 11:59 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

Command line parameters:

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Query length: 353

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Database sequences: 1472140

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ACCESSION AF034780

VERSION AF034780.1 GI:4090955

KEYWORDS

SOURCE human.

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1062)

AUTHORS MacLennan,A.J., Browe,C.S., Gaskin,A.A., Lado,D.C. and Shaw,G.

TITLE Cloning and characterization of a putative G-protein coupled receptor potentially involved in development

JOURNAL Mol. Cell. Neurosci. 5 (3), 201-209 (1994)

MEDLINE 94373324

AUTHORS

REFERENCE 2 (bases 1 to 1062)

AUTHORS An,S.

TITLE Edg5, a Human homolog of rat H218 that is a functional receptor for lysosphingolipids

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1062)

AUTHORS An,S.

TITLE Direct Submission

JOURNAL Submitted (16-NOV-1997) Medicine, UC-San Francisco, 533 Parnassus Ave., San Francisco, CA 94143-0711, USA

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REFERENCE 1 (bases 1 to 156503)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
TITLE Unpublished
REFERENCE 2 (bases 1 to 156503)
AUTHORS DOE Joint Genome Institute.
JOURNAL Direct Submission
TITLE Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
REFERENCE 3 (bases 1 to 156503)
AUTHORS DOE Joint Genome Institute and Stanford Human Genome Center.
JOURNAL Direct Submission
TITLE Submitted (15-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell
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COMMENT On Aug 15, 2001 this sequence version replaced gi:14971180.
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www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
www.shgc.stanford.edu
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US-09-274-752D-3 x AC011511

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116456 ATGGGCAGCTGTGTACTCGAGTACTGAACCCACAAAGGTCCAGGAACA 117005
17 sTyrAsnTyrThrLysGluThrLeuGluThrGlnGluThrThrSerArg 34
117005 CTATAATTATACCAAGGAGAGCGTGGAAACCGCAGGAGACGCTCCGCC 117055
34 lnValAlaSerAlaGlyIleValIleLeuCysAlaIleValValGlu 50
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```
117056 AGTGGGCTGGCTTCATCGTCATCTCTGTTGGCCATTGTGTGGAA 117105
|||||
51 AsnLeuLeuValLeuIleAlaValAlaArgAsnSerLysPheHisSerAl 67
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117106 AACCTCTGGTGCATATTGGCGGTGGCGGAGCAAGCAAGATTCCACCTCGGC 117155
|||||
67 aMetTyrLeuPheLeuGlyAsnLeuAlaAlaSerAspLeuLeuAlaGlyV 84
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117156 AATGACCTGTTCTGGGCAACCTGGCGCTCCGATCTACTGGCAGGCG 117205
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84 alAlaPheValAlaAsnThrLeuLeuSerGlySerValThrLeuArgLeu 100
|||||
117206 TGGCCTTCGTAGCAATACCTGTCTCTGGCTCTGTCCAGCTGAGGCTG 117255
|||||
101 ThrProValGlnTrpPheAlaArgCluclySerAlaSerIleThrLeuSe 117
|||||
456 ACGCCTGTGAGTGGTTGGCGGAGGGCTGTGCCTTCATCACCTCTC 117305
|||||
117 rAlaSerValGlySerLeuLeuAlaIleAlaIleGluArgHisValAlaI 134
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117306 GGCCTCTGTCTACGCTCTGGCCATCGCCATTGAGCGCCACGTGGCCA 117355
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134 leAlaLysValLysLeuTyrGlySerCysLysSerCysArgMetLeuLeu 150
|||||
117356 TTGCCAAGGTCAAGCTGTATGCGAGCAAGAGCTGCGCATGCTTCTG 117405
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151 LeuIleGlyAlaSerTrpLeuIleSerLeuValLeuGlyGlyLeuProIl 167
|||||
117406 CTCATCGGGGCTCGTGCTCATCTCGCTGTGCTGCTGCTGCTGCCAT 117455
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167 eLeuGlyTrpAsnCysLeuGlyHisLeuGluAlaCysSerThrValLeuP 184
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117456 CCTTGGCTGGAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 117505
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184 roLeuTyrAlaLysHisTyrValLeuCysValValThrIlePheSerIle 200
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117506 CTCCTACGCCCAAGCATTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 117555
|||||
201 IleLeuLeuAlaIleValAlaLeuTyrValArgIleTyrCysValValAr 217
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117556 ATCTGTGTGGCCATCGTGGCCCTGTACGTGGCATCTACTGCGTGGTCCG 117605
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217 qSerSerHisAlaAspMetAlaAlaProGlnThrLeuAlaLeuLysT 234
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234 hrValThrIleValLeuGlyValPheIleValCysTrpLeuProAlaPhe 250
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117656 CGGTACCATCGTGTAGCGCTCTTATCGTCTGCTGCTGCTGCTGCTGCT 117705
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251 SerIleLeuLeuLeuAspTyrAlaCysProValHisSerCysProIleLe 267
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117706 AGCATCTCTCTCTGGACTATGCTGTGCTGCTGCTGCTGCTGCTGCT 117755
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267 uTyrLysAlaHisTyrPhePheAlaValSerThrLeuAsnSerLeuLeuA 284
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117756 CTAAAGCCCACTACTTTTTCGCGCTCTCCACCTCGAATTCCTGCTGCT 117805
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284 snProValIleTyrThrTrpArgSerArgAspLeuArgGluValLeu 300
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117806 ACCCGTCATCTACACGTGGCGAGCCGAGCTGCGGGGAGGTGCTT 117855
|||||
301 ArgProLeuGlnCysTrpArgProGlyValGlyValGlnGlyArgArgAr 317
|||||
117856 CGGCGCTGTCAGTGTGGAGCGCGGGGTGGGGTGGCAAGGACGAGGCGG 117905
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317 qValGlyThrProGlyHisHisLeuLeuProLeuArgSerSerSerL 334
|||||
117906 GGGGGGACCCCGGCGCCACCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 117955
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334 euGluArgGlyMetHisMetProThrSerProThrPheLeuGluGlyAsn 350
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FEATURES

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117956 TGGAGAGGGGCATGCATGCCACGCTCACCACGCTTCTGGAGGCAAC 118005
351 ThrValVal 353
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118006 ACGGTGGTC 118014
seq_name: gb_htg:AC073775
seq_documentation_block:
LOCUS AC073775 214006 bp DNA HTG 18-JUL-2000
DEFINITION Mus musculus clone RP23-382B11, WORKING DRAFT SEQUENCE, 9 ordered
pieces.
ACCESSION AC073775
VERSION AC073775.2 GI:9256790
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE house mouse
ORGANISM Mus musculus
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
DOE Joint Genome Institute.
Sequencing of Mouse
Unpublished
2 (bases 1 to 214006)
DOE Joint Genome Institute.
Direct Submission
Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Jul 18, 2000 this sequence version replaced gi:8810392.
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 1883595
Center clone name: RPCI-23_382B11
-----
Summary Statistics
Consensus quality: 209197 bases at least Q40
Consensus quality: 212478 bases at least Q30
Consensus quality: 212996 bases at least Q20
Estimated insert size: 218930; agarose-fp estimation
Estimated insert size: 213656; sum-of-contigs estimation
Quality coverage: 9.1 in Q20 bases; agarose-fp estimation
Quality coverage: 9.33 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 9 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 11489: contig of 11489 bp in length
* 11490 11589: gap of unknown length
* 11590 72347: contig of 60758 bp in length
* 72348 72447: gap of unknown length
* 72448 79269: contig of 6822 bp in length
* 79270 79369: gap of unknown length
* 79370 79945: contig of 576 bp in length
* 79946 80045: gap of unknown length
* 80046 101339: contig of 21294 bp in length
* 101340 101439: gap of unknown length
* 101440 118105: contig of 16666 bp in length
* 118106 118205: gap of unknown length
* 118206 142604: contig of 24399 bp in length
* 142605 142704: gap of unknown length
* 142705 151311: contig of 8607 bp in length
* 151312 151411: gap of unknown length
* 151412 214006: contig of 62595 bp in length.
Location/Qualifiers
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source          1..214006
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-382B11"
/clone_lib="RPC1 mouse BAC library 23"
BASE COUNT     49780 a 52378 g 56332 t 800 others
ORIGIN

alignment_scores:
  Quality: 1595.50      Length: 353
  Ratio: 4.734         Gaps: 1
  Percent similarity: 95.467 Percent identity: 89.235

alignment_block:
US-09-274-752D-3 x AC073775

Align seg 1/1 to: AC073775 from: 1 to: 214006

1 MetGlySerLeuTyrSerGluTyrLeuAsnProAsnLysValGlnGluH1 17
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
13999 ATGGCGGCTTATCTACTCAGAGTACTCAATCCTGAGAGGTCTGGRACA 14048
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
17 sTyrAsnTyrThrLysGluThrLeuGluThrGlnGluThrThrSerArg 34
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
J49 CTACAATTACACCAAGAGAGAGCTGGACATGCAGGAGACCACCTCCCGCA 14098
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
34 InValAlaSerAlaGlyLeuValLeuLysCysAlaIleValValGlu 50
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14099 AGGTGGCTGGCTTCATCATCATCTGTGCTGGCCATCGTGGTGAG 14148
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
51 AsnLeuLeuValLeuIleAlaValAlaArgAsnSerLysPheHisSerAl 67
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14149 AATCTTCTGGTGCTCATTCAGTGGCCAGGAGAACAGCAATTCCTCAGC 14198
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
67 aMetTyrLeuPheLeuGlyAsnLeuAlaAlaSerAspLeuLeuAlaGly 84
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14199 AATGTACTGTCTCTGGCAACCTGGCAGCCTCTGACCTGTGGCAGGCG 14248
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
84 alaIlePheValAlaAsnThrLeuLeuSerGlySerValThrLeuArgLeu 100
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14249 TGGCTTCTGGTGGCCAAACCTTACTCTCAGGGCATGTCTGCTGCTTA 14298
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101 ThrProValGlnTrpPheAlaArgGluGlySerAlaSerIleThrLeuSe 117
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117 rAlaSerValGlySerLeuLeuAlaIleAlaIleGluArgHisValAlaI 134
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14349 CGCCTCGGCTTTAGCCTCTCTGGCCATCGCCATCGAGAGCAAGTGGCC 14398
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134 leAlaLysValLysLeuTyrGlySerCysLysSerCysArgMetLeuLeu 150
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
99 TCGGCAAGGTCAAGCTCTACGGCAGTGCACAAAGCTGCCGAATGCTGATG 14448
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
151 LeuIleGlyAlaSerTrpLeuIleSerLeuValLeuGlyGlyLeuProIl 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14449 CTCATCGGGGCTCTTGGCTCATATCGCTGATTCGGTGGCTGCCCAT 14498
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
167 eLeuGlyTrpAsnCysLeuGlyHisLeuGluAlaCysSerThrValLeuP 184
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14499 CCTGGCTGGAATGTCTGAACAGCTGGAGGCTGCTCCACCGTGTGC 14548
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
184 roLeuTyrAlaLysHisTyrValLeuCysValValThrIlePheSerIle 200
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14549 CTCCTATGTGAAGCACTACGTGCTCTGGTGGTCCACCATCTCTCCGTC 14598
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
201 IleLeuLeuAlaIleValAlaLeuTyrValArgIleTyrCysValValAr 217
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14599 ATCTTACTGGCTATGCTGGCTGCTGATACGTCGGAATCTACTTGTAGTCCG 14648
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
217 gSerSerHisAlaAspMetAlaAlaProGlnThrLeuAlaLeuLeuLysT 234
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

```

14649 CTCGAGCCACGCGGATGTTGCTGCTCTCAGACGCTAGCCCTGCTCAGA 14698
234 hrValThrIleValLeuGlyValPheIleValCysTrpLeuProAlaPhe 250
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14699 CGGTCAACCATGCTACTGGGTGTTTTCATCATCTGCTGGCTGCCGCTTT 14748
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
251 SerIleLeuLeuLeuAspTyrAlaCysProValHisSerCysProIleLe 267
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14749 AGCATCCCTCTCTAGACTCCACCTGTCCCGTTCGGGCTGCCCTGTCT 14798
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267 uTyrLysAlaHisTyrPhePheAlaValSerThrLeuAsnSerLeuLeu 284
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14799 CTACAAAGCCCACTATTTTGGCTTGGCCACCTTAACTCAGCTGCTCA 14848
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
284 snProValIleTyrThrTrpArgSerArgAspLeuArgArgGluValLeu 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14849 ATCTGTCTCATATACGTGGGTGACCGGGACCTTCGGAGGGAGGTGCTG 14898
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
301 ArgProLeuGlnCysTrpArgProGlyValGlyValGlnGlyArgArgAr 317
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14899 CGGCCCCGTGCACTGTGGCGGAGAGGAAGGAGTGACGGGACCGCAGAG 14948
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317 gValGlyThrProGlyHisHisLeuLeuProLeuArgSerSerSerLe 334
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14949 T...GGGAACCTGTGTCACCGACTCTGCTCTCCGACGCTCCAGCTCC 14995
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334 euGluArgGlyMethHisMetProThrSerProThrPheLeuGluGlyAsn 350
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
14996 TGGAGAGAGGCATGCTATGCTATACCATCCGACATTTCTGGAGGGTAAC 15045
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
351 ThrValVal 353
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15046 ACAGTGGTCC 15054
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seq_name: gb_htg.AC073781

seq_documentation_block:
LOCUS      AC073781 220103 bp DNA HTG 02-SEP-2000
DEFINITION Mus musculus clone RP23-398A12, WORKING DRAFT SEQUENCE, 13 ordered
            pieces.
ACCESSION  AC073781
VERSION    AC073781.2 GI:9964815
KEYWORDS   HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE     house mouse.
ORGANISM   Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  1 (bases 1 to 220103)
AUTHORS   DOE Joint Genome Institute.
TITLE     Sequencing of Mouse
JOURNAL   Unpublished
          2 (bases 1 to 220103)
AUTHORS   DOE Joint Genome Institute.
TITLE     Direct Submission
JOURNAL   Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
          Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT    On Sep 2, 2000 this sequence version replaced gi:8810398.
          -----Genome Center
          Center: Joint Genome Institute
          Center Code: JGI
          Web site: http://www.jgi.doe.gov
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          Project Information
          Center Project Name: 1889716
          Center clone name: RPCI-23_398A12
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          Summary Statistics
          Consensus quality: 209550 bases at least Q40
          Consensus quality: 216439 bases at least Q30
          Consensus quality: 217881 bases at least Q20
          Estimated insert size: 22880; agarose-fp estimation
          sum-of-contigs estimation
          Quality coverage: 6.87 in Q20 bases; agarose-fp estimation

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Quality coverage: 6.98 in Q20 bases; sum-of-contigs estimation.

* NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

* This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

- 40803: contig of 40803 bp in length
- 40804: gap of unknown length
- 40904: contig of 620 bp in length
- 41523: gap of unknown length
- 41623: gap of unknown length
- 41624: contig of 14088 bp in length
- 55712: gap of unknown length
- 55812: contig of 6001 bp in length
- 61813: gap of unknown length
- 61912: contig of 55694 bp in length
- 61913: gap of unknown length
- 117607: contig of 4567 bp in length
- 117707: gap of unknown length
- 122274: contig of 1029 bp in length
- 123403: gap of unknown length
- 123404: contig of 1291 bp in length
- 123503: gap of unknown length
- 124794: contig of 3072 bp in length
- 124894: gap of unknown length
- 127965: contig of 22714 bp in length
- 128066: gap of unknown length
- 150780: contig of 19773 bp in length
- 150880: gap of unknown length
- 170653: contig of 42763 bp in length
- 213515: gap of unknown length
- 213616: contig of 6488 bp in length.

FEATURES.
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/db_xref="taxon:10090"
/clone="RP23-398A12"
/clone_lib="RPCI mouse BAC library 23"
BASE COUNT 52227 a 54487 c 54185 g 57993 t 1211 others

a' ment_scores: Length: 353
Quality: 1595.50
Ratio: 4.734
Percent Similarity: 95.467 Percent Identity: 89.235

alignment_block:

US-09-274-752D-3 x AC073781

Align seg 1/1 to: AC073781 from: 1 to: 220103

- 1 MetGlySerLeuTyrSerGluThrLeuAsnProAsnLysValGlnGluHi 17
- 173314 ATGGGGGGCTTACTACAGTACCTCAATCTCTGAGAAGTCTTGAACA 173363
- 17 tTyrAsnTyrThrLysGluThrLeuGluThrGlnGluThrSerArgG 34
- 173364 CTACAATTACCAAGGACGCTGGACATGTCAGGAGACCACTCCCGCA 173413
- 34 InValAserAlaGlyIleValIleLeuCysCysAlaIleValGlu 50
- 173414 AGGTGGCCCTTCATCATCATCTTGTGCTGCCCATCGTGGGAG 173463
- 51 AsnLeuValLeuIleAlaValAlaArgAsnSerLysPheHisSerAl 67
- 173464 ATCTCTGGTCTCATTGCGAGTGCAGCAAGCAAGTTCACCTCAGC 173513
- 67 aMetTyrLeuPheLeuGlyAsnLeuAlaAlaSerAspLeuAlaGlyV 84

seq_name: gb_ro:AF022138
seq_documentation_block:

- 173514 AATGTACCTGTTCCTTGGCAACCTGGCAGCCTCTGACCTGCTGGCGAGCGG 173563
- 84 aAlaPheValAlaAlaAsnThrLeuLeuSerGlySerValThrLeuArgLeu 100
- 173564 TGGCCCTCTGTCGCCAACACCTTACTCTCAGGGCAATGCTACTCTGCTTFA 173613
- 101 ThrProValGlnTrpPheAlaArgGluGlySerAlaSerIleThrLeuSe 117
- 173614 ACTCCGCTGACGTGGTTCGCCGAGAGGGTTCGCCCTTCATCAGCGCTC 173663
- 117 rAlaSerValGlySerLeuLeuAlaIleAlaIleGluArgHisValAlaI 134
- 173664 CCGCTCGGTCTTTCAGCTCCTCGCCATCGCCATCGAGACAAAGTGCCGC 173713
- 134 leAlaLysValLysLeuTyrGlySerCysLysSerCysArgMetLeuLeu 150
- 173714 TGGCCAGGTCAAGCTCTACGGCAGTGCACAAAGCTGCCGAATGCTGATG 173763
- 151 LeuIleGlyAlaSerTrpLeuIleSerLeuValLeuGlyGlyLeuProII 167
- 173764 CTCATCGGGGCTCTTGGCTGATATCGCTGATTCTGGTGGCTTGCCTAT 173813
- 167 eLeuGlyTrpAsnCysLeuGlyHisLeuGluAlaCysSerThrValLeuP 184
- 173814 CCGTGGCTGGAATTGTCTGAACAGCTGGAGGCTGCTCCACCGTGTGTC 173863
- 184 rLeuTyrAlaLysHisTyrValLeuCysValValThrIlePheSerIle 200
- 173864 CTCTCTATGCTAAGCACTAGTGTCTGCGGTGTCACCATCTCTCCGCT 173913
- 201 IleLeuLeuAlaIleValAlaLeuTyrValArgIleTyrCysValValAr 217
- 173914 ATCTTACTGGCTATCGTGGCTCTGACGTCGGAATCTACTTGTAGTCCG 173963
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- 173964 CTCACGCCACGCGGATGTTGCTGCTCAGACGCTAGCCCTGCTCAAGA 174013
- 234 hrValThrIleValLeuGlyValPheIleValCysTrpLeuProAlaPhe 250
- 174014 CGGTACCATCGTACTGGGTGTTTTCATCATCTGCTGGCTGCGCGCTTTT 174063
- 251 SerIleLeuLeuLeuAspTyrAlaCysProValHisSerCysProIleLe 267
- 174064 AGCATCTCTCTTAGACTCCACTGTCCTGTCCTGGCGCTGCTGCTGCTCT 174113
- 267 uTyrLysAlaHisTyrPhePheAlaValSerThrLeuAsnSerLeuAla 284
- 174114 CTACAAAGCCCACTATTTTGGCTTTGCCACCCCTTAACCTCACTGTCA 174163
- 284 snProValIleTyrThrTrpArgSerArgAspLeuArgGluValLeu 300
- 174164 ATCCTGTCTATCTATACGTGGCTAGCGGACCTTCGGAGGAGGTGCTG 174213
- 301 ArgProLeuGlnCysTrpArgProGlyValGlyValGlnGlyArgArgAr 317
- 174214 CGGCCCTCGAGTCTGGCGAGGAGGAGGTGAGTACGGGACCGACAGG 174263
- 317 gValGlyThrProGlyHisHisLeuLeuProLeuArgSerSerSerL 334
- 174264 T....GGAACCCCTGGTCAACGACTCCCTCCGCTCTCCGAGCTCCAGTCCC 174310
- 334 euGluArgGlyMetHisMetProThrSerProThrPheLeuGluGlyAsn 350
- 174311 TGGAGAGAGCATGCATATGCTATACATCAGCAGCATTTCTGGAGGTAAC 174360
- 351 ThrValVal 353
- 174361 ACAGTGGTC 174369


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DEFINITION   DNA encoding a peptide that has receptor activity coupling with
              GTP-binding protein.
ACCESSION    E07989
VERSION      E07989.1 GI:2176120
KEYWORDS     JP 1994234797-A/1.
SOURCE       Homo sapiens.
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 1139)
AUTHORS      Takuwa,A.
TITLE        NEW PEPTIDE HAVING RECEPTOR ACTIVITY AND DNA ENCODING THE PEPTIDE
JOURNAL      Patent: JP 1994234797-A 1 23-AUG-1994;
              TSUMURA & CO, TAKUWA AKIRA
COMMENT      OS Homo sapiens (human)
              PN JP 1994234797-A/1
              PD 23-AUG-1994
              PF 10-FEB-1993 JP 1993044330
              PI TAKUWA AKIRA
              PC C07K13/00,C07H21/04,C12N15/12,C12P21/02;
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              CC topology: Linear;
              FH Key
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              FT /organism='Homo sapiens'
              FT 37..1095
              FT CDS
              FT /product='a peptide that has receptor activity
              FT coupling
              FT with GTP-binding protein'.
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              /db_xref='taxon:9606'
BASE COUNT   210 a 359 c 295 g 275 t
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  Ratio: 4.745          Gaps: 1
  Percent Similarity: 94.901 Percent Identity: 88.669
alignment_block:
  US-09-274-752D-3 x E07989
  Align seg 1/1 to: E07989 from: 1 to: 1139
1 MetGlySerLeuTyrSerGluTyrLeuAsnProAsnLysValGlnGluHi 17
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37 ATGGGCGGTTTATCTACAGAGTACCTCAATCCTCAGAAAGCTTCAGGAACA 86
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
17 sTyrAsnTyrThrLysGluThrLeuGluThrGlnGlnGluThrSerArg 34
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AUTHORS       Gonda,K. and Takuwa,Y.
TITLE         Direct Submission
JOURNAL       Submitted (13-AUG-1998) to the DDBJ/EMBL/GenBank databases. Koichi
Gonda, University of Tokyo, Molecular and Cellular Physiology;
Hongo 7-3-1, Bunkyo-ku, Tokyo 113-0033, Japan
(E-mail:gonda@u-tokyo.ac.jp, Tel:81-3-3812-2111,
Fax:81-3-5800-6845)
REFERENCE     2 (sites)
AUTHORS       Okazaki,H., Ishizaka,N., Sakurai,T., Kurokawa,K., Goto,K.,
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TITLE         Molecular cloning of a novel putative G protein-coupled receptor
expressed in the cardiovascular system
JOURNAL       Biochem. Biophys. Res. Commun. 190 (3), 1104-1109 (1993)
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DEFINITION cds.
ACCESSION U10699
VERSION U10699.1 GI:505647
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Rattus.
REFERENCE 1 (bases 1 to 2754)
AUTHORS MacLennan,A.J., Browe,C.S., Gaskin,A.A., Lado,D.C. and Shaw,G.
TITLE Cloning and characterization of a putative G-protein coupled
receptor potentially involved in development
JOURNAL Mol. Cell. Neurosci. 5, 201-209 (1994)
MEDLINE 94373324
REFERENCE 2 (bases 112 to 1250)
AUTHORS Okazaki,H., Ishizaka,N., Sakurai,T., Kurokawa,K., Goto,K.,
Kumada,M. and Takuwa,Y.
TITLE Molecular cloning of a novel putative G protein coupled receptor
expressed in the cardiovascular system
JOURNAL Biochem. Biophys. Res. Commun. 190, 1104-1109 (1993)
MEDLINE 93176155
REFERENCE 3 (bases 1 to 2754)
AUTHORS MacLennan,A.J.
TITLE Direct Submission
JOURNAL Submitted (14-JUN-1994) MacLennan A. J., University of Florida,
Neuroscience, 1600 S.W. Archer Road, Gainesville, FL 32610, USA
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VERSION AF108020.1 GI:4324650
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REFERENCE 1 (bases 1 to 1059)
AUTHORS Zhang, G., Contos, J.J., Weiner, J.A., Fukushima, N. and Chun, J.
TITLE Comparative analysis of three murine G-protein coupled receptors
activated by sphingosine-1-phosphate
Gene 227 (1), 89-99 (1995)
JOURNAL 99132320
MEDLINE
REFERENCE 2 (bases 1 to 1059)
AUTHORS Zhang, G., Contos, J.J.A. and Chun, J.
TITLE Direct Submission
JOURNAL Submitted (20-NOV-1998) Pharmacology, School of Medicine,
University of California at San Diego, 9500 Gilman Drive, La Jolla,
CA 92093-0636, USA
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REFERENCE
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  Kupperman,E., An,S., Osborne,N., Waldron,S. and Stainier,D.Y.
  A sphingosine-1-phosphate receptor regulates cell migration during
  vertebrate heart development
  JOURNAL Nature 406 (6792), 192-195 (2000)
  MEDLINE 20365730
  REFERENCE
  2 (bases 1 to 1110)
  Kupperman,E., An,S., Osborne,N., Waldron,S. and Stainier,D.Y.R.
  Direct Submission
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297  ArgGluValLeuArgProLeuGlnCysTrpArgProGlyValGlyValGI 313
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
949  AAGGATTTCTTGGAGGCTCTGTGTGCTGG..... 978
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
313  nGlyArgArgValGlyThrProGlyHisHis.....LeuLeuProLeuA 329
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979  .GGCTGCTCAATTGCGGAGACCTCTCCACCTGCTGATGTATACCATCA 1027
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329  rgSerSerSerSerLeuGlu 335
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LOCUS AF289992 607 bp mRNA ROD 02-AUG-2001
DEFINITION Cavia porcellus endothelial differentiation sphingolipid
G-protein-coupled receptor 5 mRNA, partial cds.
ACCESSION AF289992
VERSION AF289992.1 GI:15077230
KEYWORDS
SOURCE domestic guinea pig.
ORGANISM Cavia porcellus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Hystricognathi; Cavidae; Cavia.
REFERENCE 1 (bases 1 to 607)
AUTHORS Segura,B.J., Xiao,L., Cowles,R.A., Turner,D.J., Logsdon,C.D. and
Mulholland,M.W.
TITLE Sphingosine-1-phosphate Mediates Calcium Signaling in Enteric Glia
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 607)
AUTHORS Xiao,L. and Mulholland,M.W.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-2000) Surgery, University of Michigan, 1500 E.
Medical Center Drive, Ann Arbor, MI 48109-0331, USA
FEATURES
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BASE COUNT 79 a 214 c 184 g 130 t
ORIGIN

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US-09-274-752D-3 x AF289992

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 36 aSerAlaGlyIleValIleLeuCysCysAlaIleValValIleValAla 53
 51 CTCGGCCTTCATCGTCATCTGCTGGCCATCGTGGTGGAACCTGC 100
 53 euValLeuIleAlaValAlaArgAsnSerLysPheHisSerAlaMetTyr 69
 101 TGGTGCTGCTCGCGGTGGCGGACAGCAAGCTGCACCTCGGCATGTAT 150
 70 LeuPheLeuGlyAsnLeuAlaAlaSerAspLeuLeuAlaGlyValAlaPh 86
 151 GTCTTCTCGGCAACCTGGCGGCTCCGACCTCTGGCGGCGTGGCCTT 200
 86 eValAlaAsnThrLeuLeuSerGlySerValThrLeuArgLeuThrProv 103
 201 CATCGCCACACCTTCTGCTGGGGCTCCGTCACCCCTGCACCTGACGCGG 250
 103 aGlnTrpPheAlaArgGluGlySerAlaSerIleThrLeuSerAlaSer 119
 251 TGGAGTGGTTCGCCCGCGAGGGCTCGGCTTCATCAGCTGTCCGCTCC 300
 120 ValGlySerLeuLeuAlaIleAlaIleGluArgHisValAlaIleAlaTy 136
 301 GTCTTCAGCCTCTCGCCATCGCCATCGAGCGCACGTGGCCATCGCAA 350
 136 sValLysLeuTyrGlySerCysLysSerCysArgMetLeuLeuLeuIleG 153
 351 GGTCAAGCTGTACGGCAGGACGAAGAGCTGCCGACGTGCTGCTCATCG 400
 153 lYAlaSerTrpLeuIleSerLeuValLeuGlyGlyLeuProIleLeuGly 169
 401 GGGCTCATGGGTATCTTGTGGTCTCTGGGGGCTCCCATCTCTGGGC 450
 170 TrpAsnCysLeuGlyHisLeuGluAlaCysSerThrValLeuProLeuTy 186
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 186 rAlaLysHisTyrValLeuCysValValThrIlePheSerIleIleLeuL 203
 501 CCCCAGCAGTACGTGCTGTGGTGACCATCTACTGTGTGGTCCGCTCCAGC 550
 203 euAlaIleValAlaLeuTyrValArgIleTyrCysValValArgSerSer 219
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seq_name: gb_ro:AF090995

seq_documentation_block:

LOCUS AF090995 573 bp mRNA ROD 19-OCT-2000
 DEFINITION Rattus norvegicus putative G-protein coupled receptor (GPCR18)
 mRNA, partial cds.

ACCESSION AF090995

VERSION AF090995.1 GI:10880457

KEYWORDS

SOURCE

ORGANISM

Norway rat.
 Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 573)
 Caroll,S.L., Miller,M.L. and Benedict-Hamilton,H.M.
 Identification and characterization of novel G-protein coupled

receptors expressed in regenerating peripheral nerve
 Unpublished

JOURNAL 2 (bases 1 to 573)

AUTHORS Carroll,S.L., Miller,M.L. and Benedict-Hamilton,H.M.

TITLE Direct Submission

JOURNAL Submitted (11-SEP-1998) Pathology, University of Alabama at
 Birmingham, LHRB513, 701 South 19th Street, Birmingham, AL
 35294-0007, USA

FEATURES Location/Qualifiers

Source

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BASE COUNT 90 a 184 c 133 g 166 t

ORIGIN

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Quality: 850.00 Length: 190

Ratio: 4.722 Gaps: 0

Percent similarity: 94.737 Percent Identity: 87.895

alignment_block:

US-09-274-752D-3 x AF090995

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 110 ySerAlaSerIleThrLeuSerAlaSerValGlySerLeuLeuAlaIleA 127
 52 TTCAGCCTTCATCAGCGTCTCTGCGTCTTCAGCTCTCGCCATTG 101
 127 lalIleGluArgHisValAlaIleAlaLysValLysLeuTyrGlySerCys 143
 102 CCATCGAGAGACAGTGGCCATCCCAAGGTCAAGCTCTACGGCAGTGAC 151
 144 LysSerCysArgMetLeuLeuLeuIleGlyAlaSerTrpLeuIleSerLe 160
 152 AAAAGCTGTCGAATGTTGATGCTCATTTGGGGCCTCTTGGCTGATATCGCT 201
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 202 GATTCTGGTGGCTTGGCCATCTCTGGCTGGAATGCTGGACCATCTGG 251
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 194 ValValThrIlePheSerIleLeuLeuAlaIleValAlaLeuTyrVa 210
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 210 lArgIleTyrCysValValArgSerSerHisAlaAspMetAlaAlaProG 227
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452 ATCTGCTGGCTGGCGGCTTTTAGCATCCCTTCTTAGACTCTACCTGTCC 501
260 oValHisSerCysProIleLeuTyrLysAlaHisTyrPhePheAlaVals 277
502 CGTCCGGGCTGTCCCTGTCCCTACAAAGCCCATTTATTTCTTGGCCTTCG 551
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Date: Dec 20, 2001 11:57 AM

About: Results were produced by the GenCore software, version 4.5,
Copyright (c) 1993-2000 CompuGen Ltd.

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-QGAPEXT=0.050 -XGAPOP=10.000 -XGAPEXT=0.500 -FGAPOP=6.000
-DELEXT=7.000 -START=1 -MATRIX=blosum62 -TRANS=human40.cdi
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Search information block:

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Database: GenEmbl.*

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Database length: -341344837

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DEFINITION Sequence 6 from Patent WO0112838.
ACCESSION AX085543
VERSION AX085543.1 GI:13275577
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1734)
AUTHORS Erickson,J., Goddard,J.G., Kiefer,M. and Picker,D.
TITLE Compounds which modulate the activity of an lpa receptor
JOURNAL Patent: WO 0112838-A 6 22-FEB-2001;
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LOCUS AF233092 Homo sapiens lysophosphatidic acid G protein-coupled receptor 4

DEFINITION (EDG4) mRNA, complete cds.

ACCESSION AF233092

VERSION AF233092.1 GI:7243675

KEYWORDS

SOURCE human:

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1159)

AUTHORS Bandoh,K., Aoki,J., Taira,A., Tsujimoto,M., Arai,H. and Inoue,K.

TITLE Lysophosphatidic acid (LPA) receptors of the EDG family are differentially activated by LPA species. Structure-activity relationship of cloned LPA receptors

JOURNAL FEBS Lett. 478 (1-2), 159-165 (2000)

MEDLINE 20382744

REFERENCE 2 (bases 1 to 1159)

AUTHORS Bandoh,K., Aoki,J., Taira,A., Tsujimoto,M., Arai,H. and Inoue,K.

TITLE Direct Submission

JOURNAL Submitted (09-FEB-2000) Graduate School of Pharmaceutical Sciences, The University of Tokyo, 7-3-1, Hongo, Bunkyo-ku, Tokyo 113-0033, Japan

FEATURES

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BASE COUNT 183 a 394 c 325 g 257 t

ORIGIN

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Quality: 1952.00 Length: 383

Ratio: 5.110 Gaps: 1

Percent Similarity: 99.739 Percent Identity: 99.478

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US-09-274-752D-1 x AF233092

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7 ATGGTCATCATGGGCCAGTCTACTACAGAGAGACCATCGGCTTCTTCTA 56

17 rAsnAspSerGlyLysGluLeuSerSerHisTrpArgProLysAspValV 34

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57 TACAACAGTGGCAAGAGCTCAGCTCCACTGGCGGCCCAAGGATGTGG 106

34 alValValAlaLeuGlyLeuThrValSerValLeuValLeuLeuThrAsn 50

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107 TCGTGGTGGCAGCTGGGGCTGACCGTACGCGTGGTGGTGGTGGTGGTGG 156

51 LeuLeuValIleAlaIleAlaSerAsnArgArgPheHisGlnProIle 67
157 CTGCTGGTCATAGCAGCATCGCTCCCAACCGCGCTTCCACGAGCCAT 206
67 eTyrTyrLeuLeuGlyAsnLeuAlaAlaAspLeuPheAlaGlyVala 84
207 CTACTACCTGCTGGCAATTCGGCGCGGTGACCTCTTGGCGGGGTGG 256
84 IaTyrLeuPheLeuMetPheHisThrGlyProArgThrAlaArgLeuSer 100
257 CCTACCTCTTCCTCATGTTCCACACTGGTCCCGCAGCAGCCGACTTCA 306
101 LeuGluGlyTrpPheLeuArgGlnGlyLeuLeuAspThrSerLeuThrAl 117
307 CTTGAGGGCTGGTTCCTGCGGAGGGCTGCTGGACACAGCCCTCACTGC 356
117 aSerValAlaThrLeuLeuAlaIleAlaValGluArgHisArgSerValM 134
357 GTCGGTGGCCACACTGCTGGCCATCGCGGTGGAGCGCAGCGAGTGTGA 406
134 eAlaValGlnLeuHisSerArgLeuProArgGlyArgValValMetLeu 150
107 TGGCGGTGCAGCTGCACAGCGCGCTGCCCGTGGCGGTGCTCATGCTC 456
151 IleValGlyValTrpValAlaAlaLeuGlyLeuGlyLeuProAlaHis 167
457 ATTGTGGCGCTGTGGGTGGTGGCTGCCCTGGCGCTGGCGGTGCTGCCT 506
167 sSerTrpHisCysLeuCysAlaLeuAspArgCysSerArgMetAlaProL 184
507 CTCTGGCACTGCTCTGCTGCCCTGGAGCGCTGCTCACGATGCACCC 556
184 euLeuSerArgSerTyrLeuAlaValTrpAlaLeuSerSerLeuVal 200
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657 GCAGTGCAGCGCATGCAGACATGTCAGCTGCCACCGCGCTACCGAG 706
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267 yCysGluSerCysAsnValLeuAlaValGluLysTyrPheLeuLeuAla 284
807 CTGTGAGTCTGCAATGCTGCTGGTGTAGAAAGTACTTCTCTACTGTT 856
284 IaGluAlaAsnSerLeuValAsnAlaAlaValTyrSerCysArgAspSer 300
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301 GluMetArgArgThrPheArgArgLeuLeuCysCysAlaCysLeuArgG 317
907 GAGATGCGCGCACCTTCCGCGCGCTTCTGCTGCTGCTGCTGCTGCTG 956
317 nSerThrArgGluSerValHisTyrThrSerSerAlaGlnGlyAlaAs 334
957 GTCCACCGCGAGTCTCTCCACTATACATCTCTGCGCAGGAGGTGCCA 1006
334 eThrArgIleMetLeuProGluAsnGlyHisProLeuMetThrProPr 350
1007 GCACTCGCATCATGCTTCCCGAGAACGCGCCACCCACTGATGAGTCCACC 1056

350 oPheSerTyrLeuGluLeuGlnArgTyrAlaAlaSerAsnLysSerThrA 367
1057 CTTTACCTTACCTTGAACCTTCAGCGGTACGGCAAGCAACAATCCACAG 1106
367 LaProAspLeuTrpValLeuLeuAlaGlnProAsnGlnGlnAsp 382
1107 CCCCTGATGACTTGGGGTGTCTCTGGCTCAACCCCAACACAGGAC 1153

seq_name: gb_pr:AF197929

seq_documentation_block:

LOCUS AF197929 1810 bp mRNA PRI 01-NOV-2000
DEFINITION Homo sapiens short form lysophosphatidic acid receptor EDG4 (EDG4)
mrna, complete cds.

ACCESSION AF197929
VERSION AF197929.1 GI:11066253

KEYWORDS

SOURCE human

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 1810)

AUTHORS An,S., Bleu,T., Hallmark,O.G. and Goetzl,E.J.

TITLE Characterization of a novel subtype of human G protein-coupled
receptor for lysophosphatidic acid

JOURNAL J. Biol. Chem. 273 (14), 7906-7910 (1998)

MEDLINE 98192573

PUBMED 9525886

REFERENCE 2 (bases 1 to 1810)

AUTHORS An,S.

TITLE Human Edg4 lysophosphatidic acid receptor cDNA encoding a putative
protein with COOH-terminus different from the previously-reported
Edg4

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 1810)

AUTHORS An,S.

TITLE Direct Submission

Submitted (22-OCT-1999), Medicine, UCSF, 533 Parnassus, Room Ub-8,
San Francisco, CA 94143-0711, USA

JOURNAL Location/Qualifiers

FEATURES

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BASE COUNT 348 a 561 c 514 g 387 t

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Ratio: 5.108

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Percent Identity: 99.217

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US-09-274-752D-1 x AF197929

Length: 383

Gaps: 1

Align seg 1/1 to: AF197929 from: 1 to: 1810 **CFV**

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34 alValValAlaLeuGlyLeuThrValSerValLeuValLeuLeuThrAsn 50
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51 LeuLeuValIleAlaAlaIleAlaSerAsnArgPheHisGlnProII 67
269 CTGCTGGTATAGCAGCCATCGCTCCAAACCGCGCTTCCACAGGCCAT 318
67 eTyrTyrLeuLeuGlyAsnLeuAlaAlaAlaAspLeuPheAlaGlyVal 84
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84 lAtyTyrLeuPheLeuMetPheHisThrGlyProArgThrAlaArgLeuSer 100
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101 LeuGluGlyTyrPheLeuArgGlnGlyLeuLeuAspThrSerLeuThrAl 117
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117 aserValAlaThrLeuLeuAlaIleAlaValGluArgHisArgSerValM 134
469 GTCGCTGGCCACACTCTGGCCATCGCGCTGGAGCGGCGACCGAGTGA 518
134 eTAlaValGlnLeuHisSerArgLeuProArgGlyArgValValMetLeu 150
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151 lIleValGlyValTrrPheValAlaAlaLeuGlyLeuGlyLeuLeuProAlaH 167
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167 sSerTrrPheHisCysLeuCysAlaLeuAspArgCysSerArgMetAlaProL 184
619 CTCTGCGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 668
184 eLeuSerArgSerTyrLeuAlaValTrrPheAlaLeuSerSerLeuLeuVal 200
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719 TTCTGCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 768
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769 GCGAGTGCAGAGATGCGCAGAGATGTCAGCTGCCACCCCGCTTACCGAG 818
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317 nSerThrArgGluSerValHisTyrThrSerSerAlaGlnGlyGlyAla 334
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1169 CTTTAGTACTTGAACCTTCAGCGTACGCGGCAAGCAACAATCCACAG 1218
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seq_documentation_block:
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 DEFINITION Macaca fascicularis brain cDNA clone:Qtra-12246, full insert sequence.

ACCESSION AB060872
 VERSION AB060872.1 GI:13874529
 KEYWORDS oligo capping; fis (full insert sequence).
 SOURCE Macaca fascicularis adult male temporal lobe right cDNA to mRNA, clone_lib:macaque brain cDNA library Qtra clone:Qtra-12246.

ORGANISM Macaca fascicularis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae; Cercopithecinae; Macaca.

REFERENCE 1 (sites)
 Osada, N., Hida, M., Kusuda, J., Tanuma, R., Iseki, K., Hirai, M., Terao, K., Suzuki, Y., Sugano, S. and Hashimoto, K.
 Isolation of full-length cDNA clones from macaque brain cDNA libraries
 Unpublished

JOURNAL 2 (bases 1 to 2115)
 Hashimoto, K., Osada, N., Hida, M., Kusuda, J. and Sugano, S.
 Direct Submission
 Submitted (27-APR-2001) Katsuyuki Hashimoto, National Institute of Infectious Diseases, Division of Genetic Resources; 23-1, Toyama 1-chome, Shinjuku-ku, Tokyo 162-8640, Japan
 (E-mail: khashi@nih.go.jp, URL: http://www.nih.go.jp/yoken/genebank/, Tel: 81-3-5285-1111 (ex. 2120), Fax: 81-3-5285-1181)

Lab host: TOP10
 Vector: pME18S-FL3 (Acc.No. AB009864)
 R. Site1: Braiii (CAGCTGTGTG)
 R. Site2: Braiii (CAGCTGTGTG)

Description: 1st strand cDNA was primed with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was synthesized using specific 5' and 3' primers and amplified by PCR. The PCR product was digested with SfiI and size selection was performed to exclude fragments <1.5kb. The SfiI-digested PCR product was cloned into distinct Braiii sites of pME18S-FL3. XhoI sites just outside the Braiii sites can be used to isolate the cDNA insert. Libraries were constructed by oligo-capping method (Sugano et al., Institute of Medical Science, University of Tokyo).

Custom primer used for sequencing
 { 5' end primer [CTTCTGCTTAAAGCTGCG];
 3' end primer [CGACCTGCAGCTCGAGCACA] }.

FEATURES
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BASE COUNT 391 a 662 c 609 g 453 t
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Ratio: 5.034 Gaps: 1
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US-09-274-752D-1 x AB060872

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493 TAACAACAGTGGCAAGGAGCTCAGCTCTACTGGCGGCCCAAGGATGGG 542
34 alValValAlaLeuGlyLeuThrValSerValLeuValLeuLeuThrAsn 50
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543 TCGTGGTGGCACTGGGGCTGACCGTACCGTACTGGTGTCTGCTCACCATT 592
51 LeuLeuValIleAlaIleAlaSerAsnArgArgPheHisGlnProIle 67
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593 CTCCTGGTTCATAGCAGCATCGCTCCCAACCGCGCTTCCACACGCCCAT 642
67 eTyrTyrLeuLeuGlyAsnLeuAlaAlaAspLeuPheAlaGlyValA 84
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793 GTCGTGGGCCACACTGCTGGCATCGCTGTGGAGCGGCGCGCAGTGTA 842
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DEFINITION Homo sapiens DNA from chromosome 19-cosmid R3799, genomic
sequence, complete sequence.
ACCESSION AC002306
VERSION AC002306.1 GI:2213634
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens

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REFERENCE

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AUTHORS
1 (bases 1 to 38651)
Lamerdin,J.E., McCready,P.M., Adamson,A.W., Burkhardt-Schultz,K.,
Garcia,E., Kyle,A., Ramirez,M., Stillwagen,S., Garnes,J.,
Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A.,
Olsen,A.O. and Carrano,A.V.
anonymous cosmid from 19p12
JOURNAL:
Unpublished (1997)
REFERENCE
2 (bases 1 to 38651)
Lamerdin,J.E.
AUTHORS
Direct Submission
JOURNAL
Submitted (24-JUN-1997) Human Genome Center, Lawrence Livermore

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FEATURES National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
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 7382. 7632
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Quality: 1589.50      Length: 1041
Ratio: 4.161          Gaps: 3
Percent Similarity: 36.695 Percent Identity: 36.503

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alignment_block:

US-09-274-752D-1 x AC002306/rev

Align seg 1/1 to reverse of: AC002306 from: 1 to: 38651

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DEFINITION Homo sapiens chromosome 19 clone CTC-412M14, *** SEQUENCING IN
PROGRESS ***, 2 ordered pieces.

ACCESSION AC011458
VERSION AC011458.6 GI:15022005
KEYWORDS HTG; HTGS_PHASE2; HTGS_ACTIVEFIN.
SOURCE human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 105412)
DOE Joint Genome Institute and Stanford Human Genome Center.
Direct Submission
Unpublished
2 (bases 1 to 105412)
DOE Joint Genome Institute.
Direct Submission
Submitted (07-OCT-1999) production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

On Jul 26, 2001 this sequence version replaced gi:9256295.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 2 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.

* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 67802: contig of 67802 bp in length
* 67803 67902: gap of unknown length
* 67903 105412: contig of 37510 bp in length.
-----Genome Center

Center: Joint Genome Institute
Center Code: JGI
Web site: <http://www.jgi.doe.gov>

Project Information
Center Project Name: 343690
Center clone name: CTC-412M14

Summary Statistics
Consensus quality: 104543 bases at least Q40
Consensus quality: 104583 bases at least Q30
Consensus quality: 104736 bases at least Q20
Estimated insert size: 107130; agarose-fp estimation
Estimated insert size: 104798; sum-of-contigs

estimation Quality coverage: 9.42 in Q20 bases; agarose-fp
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estimation.

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BASE COUNT 26159 a 25740 c 26109 g 27304 t 100 others
ORIGIN

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Ratio: 4.161 Gaps: 3
Percent Similarity: 36.695 Percent Identity: 36.503

alignment_block:
US-09-274-752D-1 x AC011458/rev

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DEFINITION Sequence 3 from patent US 5998164.
ACCESSION AR092424
VERSION AR092424.1 GI:10019178
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 2185)
Li,Y.,Cao,L., Ni,J., Gentz,R., Bult,C.J., Sutton,G.G. III and
Rosen,C.A.
Polynucleotides encoding human G-protein coupled receptor GPR2
Patent: US 5998164-A 3 07-DEC-1999;
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Quality: 1484.50 Length: 359
Ratio: 4.582 Gaps: 6
Percent Similarity: 90.251 Percent Identity: 86.072

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US-09-274-752D-1 x AR092424
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VERSION AC073687.1 GI:8810304
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SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Mouse
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 201331)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Project Information
Center Project Name: 1789903
Center clone name: RPCI-23_138B15
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Summary Statistics
Consensus quality: 170890 bases at least Q40
Consensus quality: 185810 bases at least Q30
Consensus quality: 188737 bases at least Q20
Estimated insert size: 207000; agarose-fp estimation
Quality coverage: 8.77 in Q20 bases; agarose-fp estimation
Quality coverage: 9.17 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 36 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1007: contig of 1007 bp in length
* 1008 1107: gap of unknown length
* 1108 2256: contig of 1149 bp in length
* 2257 2356: gap of unknown length
* 3357 3666: contig of 1310 bp in length
* 3667 3766: gap of unknown length
* 3767 5071: contig of 1305 bp in length
* 5072 5171: gap of unknown length
* 5172 6676: contig of 1505-bp in length
* 6677 6776: gap of unknown length
* 6777 8071: contig of 1295 bp in length
* 8072 8171: gap of unknown length

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  Ratio: 3.538          Gaps: 6
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VERSION AJ249844.1 GI:6523553
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SOURCE African clawed frog.
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
Kimura,Y., Schmitt,A., Fukushima,N., Ishii,I., Kimura,H.,
Nebreda,A.R. and Chun,J.
Two Novel Xenopus Homologs of Mammalian LPAL/EDG-2 Function as
Lysophosphatidic Acid Receptors in Xenopus Oocytes and Mammalian
Cells
J. Biol. Chem. 276 (18), 15208-15215 (2001)
11278944
2 (bases 1 to 1941)
Nebreda,A.R.
Direct Submission
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Programme, EMBL, Meyerhofstrasse 1, 69117 Heidelberg, GERMANY
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seq_documentation_block:
LOCUS XLA249843 2053 bp mRNA VRT 01-MAY-2001
DEFINITION Xenopus laevis mRNA for lysophosphatidic acid receptor (lpalr
gene), clone 1.
ACCESSION AJ249843
VERSION AJ249843.1 GI:6523551
KEYWORDS lpalr gene; lysophosphatidic acid receptor.
SOURCE African clawed frog.
ORGANISM
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
REFERENCE
1 (bases 1 to 2053)
Kimura,Y., Schmitt,A., Fukushima,N., Ishii,I., Kimura,H.,
Nebreda,A.R. and Chun,J.
Two Novel Xenopus Homologs of Mammalian LPAL/EDG-2 Function as
Lysophosphatidic Acid Receptors in Xenopus Oocytes and Mammalian
Cells
J. Biol. Chem. 276 (18), 15208-15215 (2001)
JOURNAL
11278944
PUBMED
2 (bases 1 to 2053)
Nebreda,A.R.
AUTHORS
Direct Submission
TITLE
Submitted (29-SEP-1999) Nebreda A.R., Developmental Biology
Programme, EMBL, Meyerhofstrasse 1, 69117 Heidelberg, GERMANY
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/organism="Xenopus laevis"
/db_xref="taxon:8355"
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MSNRVVVIVVITVAIVMGAIPTSGMNCICDLEQCSNMAPLYSDSLFVIFNPLV
TEVWVLYAHIFVYVQKTRMSRSHSGPRNRRTMMSLLKTVVILVGAFLVCWTPG
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22 sGluLeuSerSerHisTrpArgProLysAspValValValAlaLeuG 39
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444 ATACCTAGCTACAGAATGGAATGCAGTCAGCAAGCTGGTGGGACTCG 493
39 lyLeuThrValSerValLeuValLeuLeuThrAsnLeuValIleAla 55
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56 AlaIleAlaSerAsnArgArgPheHisGlnProIleTyrTyrLeuLeu 72
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694 TTGACACAGGACTCATTGACACTAGCCTGCAGCGCTCAGTACCAATT 743
122 uLeuAlaIleAlaValGluArgHisArgSerValMetAlaValGlnLeuH 139
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139 isSerArgLeuProArgGlyArgValValMetLeuIleValGlyValTrp 155
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794 ACACCAAGGATGACACAGAGAGTGGTAGTAGTGTGTTGTTATCTCG 843
156 ValAlaAlaLeuGlyLeuLeuProAlaHisSerTrpHisCysLe 172
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LOCUS AR116996 2250 bp DNA PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6140060.
ACCESSION AR116996
VERSION AR116996.1 GI:14097902
KEYWORDS
SOURCE
ORGANISM Unknown.

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REFERENCE 1 (bases 1 to 2250)
AUTHORS Chun,J.J.M. and Hecht,J.H.
TITLE Cloned lysophosphatidic acid receptors
JOURNAL Patent: US 6140060-A 1 31-OCT-2000;
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Location/Qualifiers
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/organism="unknown"

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ORIGIN

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Ratio: 3.357 Gaps: 8
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US-09-274-752D-1 x AR116996

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344 ATATCTAGCACAGATGAACACACAGTGAAGAGCTGGTGTGATGGGACTGG 393
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544 TGTTCATACAGACCTAATACCGGAGACTGACTGTAGCAGCTGGCTC 593
106 LeuArgGlnGlyLeuLeuAspThrSerLeuThrAlaSerValAlaThrLe 122
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122 uLeuAlaIleAlaValGluArgHisArgSerValMetAlaValGlnLeuH 139
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139 lSerArgLeuProArgGlyArgValValMetLeuIleValGlyValTrp 155
694 ATACAGAAATGACACACCGCGCTGGTGGTGGTATGTAGTCATCTGG 743
156 ValAlaAlaLeuGlyLeuLeuLeuProAlaHisSerTrpHisCysLe 172
744 ACTATGCCATTTGTATGGTGTCTATACCCAGTGTGGCTGGAACATGCAT 793
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189 yLeuAlaValTrpAlaLeuSerSerLeuLeuValPheLeuLeuMetVal 205
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DEFINITION Mus musculus lysophosphatidic acid receptor (vzg-1) mRNA, complete cds.

ACCESSION U70622

VERSION U70622.1 GI:1655990

KEYWORDS lysophosphatidic acid receptor; G-protein coupled receptor.

SOURCE house mouse.

ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

1 (bases 1 to 2250)

RENCHE Hecht, J.H., Weiner, J.A., Post, S.R. and Chun, J.

AUTHORS Ventricular zone gene-1 (vzg-1) encodes a lysophosphatidic acid receptor expressed in neurogenic regions of the developing cerebral cortex

J. Cell Biol. 135 (4), 1071-1083 (1996)

JOURNAL 97081105

MEDLINE 2 (bases 1 to 2250)

REFERENCE Hecht, J.H., Weiner, J.A., Post, S.R. and Chun, J.

AUTHORS Direct Submission

TITLE Submitted (12-SEP-1996) Pharmacology, University of California at

JOURNAL San Diego, School of Medicine, 9500 Gilman Drive, La Jolla, CA

92093-0636, USA

FEATURES

Location/Qualifiers

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Percent Similarity: 77.717 Percent Identity: 53.804

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US-09-274-752D-1 x MMU70622

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39 lyLeuThrValSerValLeuValLeuLeuThrAsnLeuValIleAla 55

394 GCATCAGTGTGGCGTTCATCATGTGGCAATCTCTCGTGCATGGTG 443

56 AlaIleAlaSerAsnArgPheHisGlnProIleTyrTyrLeuLeuGl 72

444 GCAATCTACGTCAACCGCGCTTCCATTTCCCTATTATTACTTGTG 493

72 yAsnLeuAlaAlaAspLeuPheAlaGlyValAlaTyrLeuPheLeuM 89

494 CACCTGCTGCTGCAGACTTCTTCGTTGGTGGCTTCTCTACCTGA 543

89 etPheHisThrGlyProArgThrAlaArgLeuSerLeuGluGlyTrpPhe 105

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644 GCTGCTATTGCTATCGAGAGGCATCATCAGGTTTTCCGCGATGCGACTCC 693

139 lssArgLeuProArgGlyArgValValMetLeuIleValGlyValTrp 155

694 ATACAGCAATGAGCAACCGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGG 743

156 ValAlaAlaLeuGlyLeuGlyLeuLeuProAlaHisSerTrpHisCysLe 172

744 ACTATGGCCATGTGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 793

172 uCysAlaLeuAspArgCysSerArgMetAlaProLeuLeuSerArgSerTr 189

794 CTGTGATATCGATCTGTTCCAACTGGCACCTCTTACAGTGGTGGTGGTGG 843

189 yLeuAlaValTrpAlaLeuSerSerLeuLeuValPheLeuLeuMetVal 205

844 ACTTACTCTCTGGGCCATTTTCAACCTGGTGGTGGTGGTGGTGGTGGTGG 893

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 20, 2001, 09:15:21 ; Search time 2907.25 Seconds
(without alignments)
9839.577 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Seed: 1472140 seqs, 8248589755 residues

Total number of hits satisfying chosen parameters: 2944280

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: gb.htg.*
- 3: gb.in.*
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- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.om.*
- 20: em.or.*
- 21: em.ov.*
- 22: em.pat.*
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- 25: em.ro.*
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- 28: em.un.*
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- 31: em.htgo_inv.*
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- 33: em.htg_hum.*
- 34: em.htg_inv.*
- 35: em.htg_rod.*
- 36: em.htg_other.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1704.4	98.3	1810	9	AF197929	Homo sapi
4	1499.6	86.4	2115	9	AB060872	Macaca fa
5	1140.6	65.8	1159	9	AF233092	Homo sapi
6	885.2	51.0	38651	9	AC002306	Homo sapi
7	883.6	51.0	105412	2	AC011458	Homo sapi
8	860.4	49.6	2185	6	AR092424	Sequence
9	594	34.3	201331	2	AC073687	Mus muscu
10	572.6	33.0	5618	10	AF218844	Mus muscu
11	365.6	21.1	1543	6	AB7639	Sequence 1
12	365.6	21.1	1543	10	AF014418	Rattus no
13	364	21.0	2250	6	AR116996	Sequence
14	364	21.0	2250	10	MMU70622	Mus muscu
15	362.4	20.9	1436	10	MMU48235	Mus muscu
16	362.4	20.9	2170	10	AF090347	Rattus no
17	342.4	19.7	1552	4	BTU48236	Bos tauru
18	341.8	19.7	1631	4	U18405	Ovis arie
19	329	19.0	1576	9	HSU80811	Human lysop
20	327.4	18.9	2687	9	AK022808	Homo sapi
21	325.8	18.8	1110	6	AX085538	Sequence
22	325.8	18.8	1217	9	HSEDG2	Sequence
23	325.8	18.8	1217	9	HSU78192	Homo sapien
24	303	17.5	2462	10	HOMOLPA4	Homo sapien
25	285.8	16.5	1941	5	XLA249844	Mus muscu
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27	282	16.3	1065	9	AF236117	Homo sapi
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36	264	15.2	2374	10	AF097733	Rattus no
37	258.6	14.9	93945	2	AL603747	Danio rer
38	256.6	14.8	90500	2	AL603785	Danio rer
39	213.8	12.3	5557	10	AF272364S1	Mus muscu
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41	213.8	12.3	110000	2	AC068947_3	Continuation (4 of
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43	213	12.3	138225	2	AL139822	Homo sapi
44	196.2	11.3	978	9	AY011720	Lemur cat
45	189.8	10.9	978	10	AY011714	Myocastor

ALIGNMENTS

RESULT 1

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DEFINITION Sequence 6 from Patent WO0112838.
ACCESSION AX085543
VERSION AX085543.1 GI:13275577
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1734)
AUTHORS Erickson,J., Goddard,J.G., Kiefer,M. and Picker,D.
TITLE Compounds which modulate the activity of an lpa receptor
JOURNAL Patent: WO 0112838-A 6 22-FEB-2001;
FEATURES
Location/Qualifiers
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 LOCUS Homo sapiens short form lysophosphatidic acid receptor EDG4 (EDG4)
 DEFINITION mRNA, complete cds.
 ACCESSION AF197929
 VERSION AF197929.1 GI:11066253
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 R. JNCE
 AUTHORS An.S., Bleu,T., Hallmark,O.G. and Goetzl,E.J.
 TITLE Characterization of a novel subtype of human G protein-coupled
 receptor for lysophosphatidic acid
 JOURNAL J. Biol. Chem. 273 (14), 7906-7910 (1998)
 MEDLINE 98192573
 PUBMED 9525886
 REFERENCE 2 (bases 1 to 1810)
 AUTHORS An.S.
 TITLE Human Edg4 lysophosphatidic acid receptor cDNA encoding a putative
 protein with COOH-terminus different from the previously-reported
 Edg4
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 1810)
 AUTHORS An.S.
 TITLE Direct Submission
 JOURNAL Submitted (22-OCT-1999) Medicine, UCSF, 533 Parnassus, Room Ub-8,
 San Francisco, CA 94143-0711, USA
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 182 tggctgtgtggcactggggctgacctcagctcagctgctgggtgtgctgacctgacctgtgtg 241
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LOCUS Homo sapiens lysophosphatidic acid G protein-coupled receptor 4
DEFINITION (EDG4) mRNA, complete cds.
ACCESSION AF233092
VERSION AF233092.1 GI:7243675
KEYWORDS human.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1159)
AUTHORS Bandoh,K., Aoki,J., Taira,A., Tsujimoto,M., Arai,H. and Inoue,K.
TITLE Lysophosphatidic acid (LPA) receptors of the EDG family are differentially activated by LPA species. Structure-activity relationship of cloned LPA receptors
JOURNAL FEBS Lett. 478 (1-2), 159-165 (2000)
MEDLINE 20382744
REFERENCE 2 (bases 1 to 1159)
AUTHORS Bandoh,K., Aoki,J., Taira,A., Tsujimoto,M., Arai,H. and Inoue,K.
TITLE Direct Submission
JOURNAL Submitted (09-FEB-2000) Graduate School of Pharmaceutical Sciences, The University of Tokyo, 7-3-1, Hongo, Bunkyo-ku, Tokyo 113-0033, Japan
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RESULT 6
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DEFINITION sequence, complete sequence.
AC002306
AC002306.1 GI:2213634
HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Lamerdin,J.E., McCreedy,P.M., Adamson,A.W., Burkhardt-Schultz,K.,
Garcta,E., Kyle,A., Ramirez,M., Stillwagen,S., Garnes,J.,
Danganan,L., Bruce,R., Quan,G., Montgomery,M., Ow,D., Kobayashi,A.,
Olsen,A.O. and Carrano,A.V.
TITLE anonymous cosmid from 19p12
JOURNAL Unpublished (1997)
REFERENCE 2 (bases 1 to 38651)
AUTHORS Lamerdin,J.E.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-1997) Human Genome Center, Lawrence Livermore
National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
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RESULT 8
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LOCUS Sequence 3 from patent US 5998164.
DEFINITION AR092424
ACCESSION AR092424
VERSION AR092424.1 GI:10019178
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REF ID: 1 (bases 1 to 2185)
TORS Li,Y.,Cao,L., Ni,J., Gentz,R., Bult,C.J., Sutton,G.G. III and
Rosen,C.A.
Polynucleotides encoding human G-protein coupled receptor GPR2
Patent: US 5998164-A 3 07-DEC-1999;
Location/Qualifiers
1. 2185
Source /organism="unknown"

BASE COUNT 413 a 621 c 696 g 455 t
ORIGIN

Query Match 49.6%; Score 860.4; DB 6; Length 2185;
Best Local Similarity 97.9%; Pred. No. 3.1e-154;
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Qy 292 ctgctcggaactctggcgcggctgacct-cttcgcgggcggtggcctcttcctcat 350
Db 1097 CTCGGGCCCAATCTGTCGGGGCTGACCTCTCTTCGGGGCGGTGGCCTTACCTTTCCTCAT 1156
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RESULT 9

AC073687/c

LOCUS

DEFINITION

AC073687

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

AC073687 201331 bp DNA
Mus musculus clone RP23-138B15, WORKING DRAFT SEQUENCE, 36
unordered pieces.
AC073687
GI:8810304
HTG; HTGS_PHASE1; HTGS_DRAFT.
house mouse.
Mus musculus
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
1 (bases 1 to 201331)
DOE Joint Genome Institute.
Sequencing of Mouse

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 1 (bases 1 to 1543)
 Allard, J., Barron, S., Diaz, J., Lubetzki, C., Zalc, B., Schwartz, J.-C.
 and Sokoloff, P.
 A G-protein-coupled receptor selectively expressed in
 myelin-forming cells
 Unpublished
 2 (bases 1 to 1543)
 Allard, J., Barron, S., Schwartz, J.-C. and Sokoloff, P.
 Direct Submission
 Submitted (16-JUL-1997) U-109, INSERM, 2ter rue d'Alesia, Paris
 75014, France
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 KEYWORDS
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 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 BASE COUNT
 ORIGIN

AR116996
 Sequence 1 from patent US 6140060.
 AR116996
 AR116996.1 GI:14097902
 Unknown.
 Unknown.
 Unclassified.
 1 (bases 1 to 2250)
 Chun, J. J. M. and Hecht, J. H.
 Cloned lysophosphatidic acid receptors
 Patent: US 6140060-A 1 31-OCT-2000;
 Location/Qualifiers
 1. .2250
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MMU70622 2250 bp mRNA ROD 30-NOV-1996
LOCUS Mus musculus lysophosphatidic acid receptor (vzg-1) mRNA, complete cds.
DEFINITION
ACCESSION U70622

U70622.1 GI:1655990
lysophosphatidic acid receptor; G-protein coupled receptor.
house mouse
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2250)
Hocht,J.H., Weiner,J.A., Post,S.R. and Chun,J.
TITLE Ventricular zone gene-1 (vzg-1) encodes a lysophosphatidic acid receptor expressed in neurogenic regions of the developing cerebral cortex
J. Cell Biol. 135 (4), 1071-1083 (1996)
MEDLINE 97081105
REFERENCE 2 (bases 1 to 2250)
Hocht,J.H., Weiner,J.A., Post,S.R. and Chun,J.
AUTHORS Direct Submission
TITLE Submitted (12-SEP-1996) Pharmacology, University of California at San Diego, School of Medicine, 9500 Gilman Drive, La Jolla, CA 92093-0636, USA
JOURNAL
FEATURES Location/Qualifiers
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ORIGIN

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

QW protein - protein search, using sw model

Run on: December 20, 2001, 10:06:21 ; Search time 65.63 Seconds
(without alignments)
851.379 Million cell updates/sec

Title: US-09-274-752D-1
Perfect score: 1968
Sequence: 1 MVIMGQYYNETIGFFYNNS.....NKSTAPDDLWVLLAQPNQOD 382

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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JJ- hed: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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9: sp_phage:*
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4	1467	74.5	348	11	Q9JU06
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7	958.5	48.7	364	11	O88584
8	879	44.7	354	11	O9EQ31
9	857.5	43.6	353	4	Q9UBX5
10	849	43.1	354	4	Q9NRB8
11	842	42.8	345	11	Q9ESJ6
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13	549.5	27.9	326	6	Q9BF48
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9	857.5	43.6	353	4	Q9UBV5	Q9UBV5 homo sapien
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16	543.5	27.7	326	6	Q9BF49	Q9BF49 tragelaphus
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18	544.5	27.7	326	6	Q9BF50	Q9BF50 hippopotamu
19	544.5	27.7	326	6	Q9BF59	Q9BF59 ateles fusc

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 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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 GN EDG7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 RA Lynch K.R., Im D.-S.;
 RA "Molecular cloning of a lysophosphatidic acid receptor, LP-A3/Edg-7.";
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99419064; PubMed=10488122;
 RA Bandoh K., Aoki J., Hosono H., Kobayashi S., Kobayashi T.,
 RA Murakami-Murofushi K., Tsujimoto M., Arai H., Inoue H.;
 P' "Molecular Cloning and Characterization of a Novel Human G-protein-
 Coupled Receptor, EDG7, for Lysophosphatidic Acid.";
 J. Biol. Chem. 274:27776-27785(1999).
 DR EMBL; AF186380; AAF00530.1;
 DR EMBL; AF127138; AAD56311.1;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1
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 Db 181 PIYSRSYLWFTVSNLMAFLIMVYVIRYVVRKTNVLSPHSGSISRRRTPMKLMT 240
 QY 243 VVILGAFVVCWTPGQVLLDGLGCESCNVLAIVEKYFLLAEANSLVNAAYVSCRDSEM 302
 Db 241 VMTVLGAFVVCWTPGQVLLDGLGCESCNVLAIVEKYFLLAEANSLVNAAYVSCRDSEM 300
 QY 303 RTFRRLCCACLRQSTRE 321
 Db 301 YNTMRKMICCA-LQDSNTE 318
 QY 363 NKSTA 367
 Db 349 NKSTS 353

RESULT 10
 Q9NRB8 PRELIMINARY; PRT; 354 AA.
 AC Q9NRB8
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE G-PROTEIN COUPLED RECEPTOR EDG-7.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=20351181; PubMed=10891327;
 RA Fitzgerald L.R., Dytko G.M., Sarau H.M., Mannan I.J., Ellis C.,
 RA Lane P., Tan K.B., Wilson S., Bergsma D.J., Ames R.S., Foley J.J.,
 RA Campbell D., McMillan L., Evans N., Elshourbagy N., Tsui P.;
 RT "Identification of an EDG7 variant, HOFNH30, a G-protein-coupled
 Receptor for Lysophosphatidic Acid.";
 RL Biochem. Biophys. Res. Commun. 273:805-810(2000).
 DR EMBL; AF236117; AAF91291.1;
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1; 1
 DR PRINTS; PR00237; GPCRHOOPS.
 DR PROSITE; PS00237; G-PROTEIN_RECEPTOR_F1_1; UNKNOWN_1.
 DR PROSITE; PS0262; G-PROTEIN_RECEPTOR_F1_2; 1.
 KW Receptor.
 SQ SEQUENCE 354 AA; 40339 MW; A70ED5CFA6F7D706 CRC64;

Query Match 43.1%; Score 849; DB 4; Length 354;
 Best Local Similarity 46.8%; Pred. No. 1.9e-58;
 Matches 162; Conservative 62; Mismatches 104; Indels 18; Gaps 2;

QY 4 MGOCYNETIGFFYNNSGKELSSHW- PKDVVVVALGLTVSVLLNLLVIAAASNR 62
 Db 1 MNECHDKHMDFFNRSNTDVTDDWTKLVILCVGTFCLFFFSNLSVIAAVIKNRK 60
 QY 63 FHQPIYLLGNLAADLAFAGVAYFLFMFHTGPTARLSLEGWFLRQGLDFTSLTASVATL 122
 Db 61 FHFPFYLLANLAAADLAFAGVAYFLFMFHTGPTARLSLEGWFLRQGLDFTSLTASVATL 120
 QY 123 LAIAVERHRSVMVQLHSLRPRGRVVMVGLVGVVWVAALGLGLLPAHSHWCLCALDRCSMA 182
 Db 121 LVIAVERHMSIMRVRVHNSLTKKRVTLILLVWAIAMFMAVPTLGWNCCLNISACSSLA 180
 QY 183 PLLSRSLAVWALSLLVFLMVAVYTRIFFYVRRVQMAEHSVCHPRTYRRTTSLVKT 242
 Db 181 PIYSRSYLWFTVSNLMAFLIMVYVIRYVVRKTNVLSPHSGSISRRRTPMKLMT 240
 QY 243 VVILGAFVVCWTPGQVLLDGLGCESCNVLAIVEKYFLLAEANSLVNAAYVSCRDSEM 302
 Db 241 VMTVLGAFVVCWTPGQVLLDGLGCESCNVLAIVEKYFLLAEANSLVNAAYVSCRDSEM 300


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QY 303 RTRFRLLCC-----ACLRQSTRESVHYTSSAOG 331
| : : : : | | | | |
Db 301 YSTMKMICCFQERNLDRSRPLSTILSRDSTGSOYKEDSSOG 346
| : : : : | | | | |

RESULT 11
Q9ESJ6 PRELIMINARY; PRT; 345 AA.
AC Q9ESJ6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE PUTATIVE G PROTEIN-COUPLED RECEPTOR SNGPCR32.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-HARLAN SPRAGUE-DAWLEY;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
R "Identification and characterization of novel G-protein coupled
R receptors expressed in regenerating peripheral nerve.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF097733; AAG24262.1;
DR InterPro: IPR00276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: P000237; GPCRHHODOPS.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS0262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 345 AA; 39137 MW; CF3BEF46EB35046A CRC64;

Query Match 42.8%; Score 842; DB 11; Length 345;
Best Local Similarity 46.6%; Pred. No. 6.4e-58;
Matches 166; Conservative 64; Mismatches 110; Indels 16; Gaps 4;

QY 15 FFYNSGKELSHWR-PKDVVVAALGLVSVLVLTNLVIAAASNRFFHQPIYLLGN 73
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 3 FFYNSRNTDADEWTGTLKVLVLCVCTFCFFIFFNSLVIAAVITNRKFFPFYLLAN 62
| : : : : | : : : : | : : : : | : : : : | : : : : |

QY 74 LAADLFAGVAYFLMFHTGPTARLTSLGFWPLRGLDTSLSATSVATLLAIVERHRSV 133
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 63 LAVADFFAGIAYVLFMFNTGPKVSKTLTVNRWLLRGLDTSLSATSLANLVIAVERHRSI 122
| : : : : | : : : : | : : : : | : : : : | : : : : |

QY 134 MAVOLHSRLPRGVVVLIVGVVVAALGLGLLPAHSHWCLALDRCSMAPLSRSYLAVW 193
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 123 MRMRTHSNLTKRVTLLVWAIEMFAGVPTLGNWCLNCSACSLAPIYSRYLIFW 182
| : : : : | : : : : | : : : : | : : : : | : : : : |

C 194 ALSLLVLLMVAVYTRIFVYRRVQRMARHVSCHPRYRETTLSLVKTVVILGAFVVC 253
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 183 TVSNLLAFFIMVVVYRYMYKRYKTVLSPTSGISRRRAPMKLMKTVMTVLGAFVVC 242
| : : : : | : : : : | : : : : | : : : : | : : : : |

QY 254 WTPGVVLLDLGLGCESCNLVAVKVEYLLAEANSLVAAVYSCRDSEMRRTFRLLCCA 313
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 243 WTPGLVLLDLGLGNQCNQVHKWELLALNLSVMPITYYKDEMYNTMRKMICCA 302
| : : : : | : : : : | : : : : | : : : : | : : : : |

QY 314 CLRQSTRESVHYTSSAOGASTRIMLPENGHPMTPPFSYLE--LQRYAASNKSTA 367
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 303 -----PHDSNAERHPS---RIPSTIHSRSDTSGOYLEDISQGVQCNKSSS 345
| : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 12
Q99NQ8 PRELIMINARY; PRT; 326 AA.
AC Q99NQ8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE EDG1 (FRAGMENT).
GN EDG1.
```

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Myocastor coypus (Coypu) (Nutria).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Myocastoridae;
OC Myocastor.
OX NCBI_TaxID=10157;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL: AY011714; AAK01982.1; -.
FT NON_TER 1
FT NON_TER 326
SQ SEQUENCE 326 AA; 36357 MW; 18963183FB9742FF CRC64;

Query Match 28.3%; Score 556.5; DB 11; Length 326;
Best Local Similarity 36.6%; Pred. No. 1e-35;
Matches 121; Conservative 70; Mismatches 111; Indels 29; Gaps 6;

QY 40 LTVSVLVLTNLVIAAASNRFFHQPIYLLGNLAADLFAGVAYFLMFHTGPTARL 99
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 13 ILICLLIILENVFVLLTIWTKKFRPMYFYFIGNLALSLLAGVAYIANLLSGTTTYRL 72
| : : : : | : : : : | : : : : | : : : : | : : : : |

QY 100 SLEGWFLRQGLDTSLSATSVATLLAIVERHRSVMAVQLHSRLPRGVVVLIVGVVVAAL 159
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 73 TLVQWFLREGSMFVALSASFSLAIAIERYITMLKMLHNGSNNSRFLLSGCGWAISL 132
| : : : : | : : : : | : : : : | : : : : | : : : : |

QY 160 GLGLLPAHSHWCLALDRCSMAPLSRSYLAVWALSLLVFLMVAVYTRIFVYRRV 219
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 133 ILGGLPIMGWNCVDALPSCSTVLPYKHYILFCTVFTLLIALLIIVLCRIYSLVTRTS 192
| : : : : | : : : : | : : : : | : : : : | : : : : |

QY 220 QMA--EHVSCHPRYRETTLSLVKTVVILGAFVVCVQVVLGLDGLGC--ESCNVLA 275
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 193 RRLTRFNKASKASRSSEKSLALLKTVIIVLSAFIACWAPLFIILLD-VCKVKTCIDLY 251
| : : : : | : : : : | : : : : | : : : : | : : : : |

QY 276 VEKYVLLAEANSLVAAVYSCRDSEMRRTFRLL--CCACLROSTRESVHYTSSAOGGAS 334
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 252 KAEYELVLAVLNSGTNPVIYITNKRMRRAFIMVSCCKC-----SGG-- 294
| : : : : | : : : : | : : : : | : : : : | : : : : |

QY 335 TRIMLPENGHPMTPPFSYLELQRYAASNKS 365
| : : : : | : : : : | : : : : | : : : : | : : : : |
Db 295 -----DSAGKIKRPIIAGVEFSRKSNDSS 319
| : : : : | : : : : | : : : : | : : : : | : : : : |

RESULT 13
Q9BF48 PRELIMINARY; PRT; 326 AA.
AC Q9BF48;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
DE EDG1 (FRAGMENT).
GN EDG1.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21082082; PubMed=11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
RA O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL: AY011733; AAK02001.1; -.
FT NON_TER 1
FT NON_TER 326
SQ SEQUENCE 326 AA; 36691 MW; C3257E28D83B88FA CRC64;
```

Query Match 27.9%; Score 549.5; DB 6; Length 326;
Best Local Similarity 36.0%; Pred. No. 3.5e-35;
Matches 121; Conservative 69; Mismatches 117; Indels 29; Gaps 6;

QY 40 LTVSVLVLLTNLLVIAAIAASNRHFOPIYVLLGNLAADLFAGVAYFLFMFHTGPTARL 99
DB 13 ILCCFIILENIIVLTWKFKHRPMYFIGNLALSDLLAGVAYTANLLSGATYKL 72
QY 100 SLEGWFLRQGLDTSATVATLLAIAVERHRSVMVQLHSRLPRGRVVMVLIQVWVAAL 159
DB 73 TPAQWFLREGSMFVALSASFVSLAIAIERITMLKMKLHNGSNRFRSFLDISACWISL 132
QY 160 GLGLPAHSHWCLCALDRCSRMAPLLSRYSYLAWALSSLLVFLMVAVYTRIFFYVRRV 219
DB 133 ILGLPLMGWNCISTLPSGSTVPLXHKHVFILCTVFTLLLAIVILYCRISLVRTS 192
QY 220 QRNA--EHVSCHPRYRETTLSLVKTVIILGAFVVCWTPGQVLLDGLGC--ESCNVLA 275
DB 193 RLUTFRKNISKASRSSEKSLALKTVIILGVFIACWAPLFIILLD-VGCKVKTCDILF 251
QY 276 VEKYEFLLAANSILVNAVYSCDSEMRRTFRL--CCACLRQSTRESVHTYSSAOGAS 334
DB 252 RTEYFLVAVNSGTNPITLTKEMRRAPVRIMSCCK-----PSGDSAGKF 300
QY 335 TRIMLPENGHPLMTPTPPSYLELQRYAASNKSTAPDD 370
DB 301 TR-----PIAGMEFSRSKSDNSHPQKD 324

RESULT 14
Q9BF52
ID Q9BF52 PRELIMINARY; PRT; 326 AA.
AC Q9BF52;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE EDG1 (FRAGMENT).
GN EDG1.
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balaenopteridae; Megaptera.
OX NCBI_TaxID=9773;
RN [1]
RP SEQUENCE FROM N.A.
F MEDLINE-21082082; PubMed-11214319;
R Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011729; AAK01997.1;
FT NON_TER 1
FT 326
SQ SEQUENCE 326 AA; 36661 MW; 8886296016C185B1 CRC64;

Query Match 27.9%; Score 548.5; DB 6; Length 326;
Best Local Similarity 36.5%; Pred. No. 4.2e-35;
Matches 122; Conservative 67; Mismatches 116; Indels 29; Gaps 6;

QY 42 VSVLVLLTNLLVIAAIAASNRHFOPIYVLLGNLAADLFAGVAYFLFMFHTGPTARLSL 101
DB 15 ICCFIILENIIVLTWKFKHRPMYFIGNLALSDLLAGVAYTANLLSGATYKLTTP 74
QY 102 EGMFLRQGLDTSATVATLLAIAVERHRSVMVQLHSRLPRGRVVMVLIQVWVAALGL 161
DB 75 AQWFLREGSMFVALSASFVSLAIAIERITMLKMKLHNGSNRFRSFLDISACWISL 134
QY 162 GLPLPAHSHWCLCALDRCSRMAPLLSRYSYLAWALSSLLVFLMVAVYTRIFFYVRRVOR 221
DB 135 GGLPIMGWNCISALPSCSTVPLXHKHVFILCTVFTLLLSIVILYCRISLVRTSRR 194
QY 222 MA--EHVSCHPRYRETTLSLVKTVIILGAFVVCWTPGQVLLDGLGC--ESCNVLA 277

DB 195 LTFERNISKASRSSEKSLALKTVIILGVFIACWAPLFIILLD-VGCKVKTCDILFRT 253
QY 278 KYFLLLAANSILVNAVYSCDSEMRRTFRL--CCACLRQSTRESVHTYSSAOGASRT 336
DB 254 EYFLVAVNSGTNPITLTKEMRRAPVRIMSCCK-----PSGDSAGKFRT 302
QY 337 IMLPENGHPLMTPTPPSYLELQRYAASNKSTAPDD 370
DB 303 -----PIAGMEFSRSKSDNSHPQKD 324

RESULT 15
Q99NR2
ID Q99NR2 PRELIMINARY; PRT; 326 AA.
AC Q99NR2;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE EDG1 (FRAGMENT).
GN EDG1.
OS Dipodomys heermanni (Kangaroo rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Heteromyidae;
OC Dipodomysinae; Dipodomys.
OX NCBI_TaxID=10018;
RN [1]
RP SEQUENCE FROM N.A.
XX MEDLINE-21082082; PubMed-11214319;
RA Murphy W.J., Eizirik E., Johnson W.E., Zhang Y.P., Ryder O.A.,
O'Brien S.J.;
RT "Molecular phylogenetics and the origins of placental mammals.";
RL Nature 409:614-618(2001).
DR EMBL; AY011710; AAK01978.1;
FT NON_TER 1
FT 326
SQ SEQUENCE 326 AA; 36486 MW; FA9C24567F402E21 CRC64;

Query Match 27.7%; Score 546; DB 11; Length 326;
Best Local Similarity 40.0%; Pred. No. 6.6e-35;
Matches 112; Conservative 65; Mismatches 97; Indels 6; Gaps 4;

QY 40 LTVSVLVLLTNLLVIAAIAASNRHFOPIYVLLGNLAADLFAGVAYFLFMFHTGPTARL 99
DB 13 ILCCFIILENIIVLTWKFKHRPMYFIGNLALSDLLAGVAYTANLLSGATYKL 72
QY 100 SLEGWFLRQGLDTSATVATLLAIAVERHRSVMVQLHSRLPRGRVVMVLIQVWVAAL 159
DB 73 TPAQWFLREGSMFVALSASFVSLAIAIERITMLKMKLHNGSNRFRSFLDISACWISL 132
QY 160 GLGLPAHSHWCLCALDRCSRMAPLLSRYSYLAWALSSLLVFLMVAVYTRIFFYVRRV 219
DB 133 ILGLPIMGWNCISALPSCSTVPLXHKHVFILCTVFTLLLSIVILYCRISLVRTS 192
QY 220 QRNA--EHVSCHPRYRETTLSLVKTVIILGAFVVCWTPGQVLLDGLGC--ESCNVLA 275
DB 193 RLUTFRKNISKASRSSEKSLALKTVIILGVFIACWAPLFIILLD-VGCKVKTCDILF 251
QY 276 VEKYEFLLAANSILVNAVYSCDSEMRRTFRL--CCAC 314
DB 252 KAEYFLVAVNSGTNPITLTKEMRRAPVRIMSCCK 291

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Job time: 2340 sec

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 Date: Dec 20, 2001 12:02 PM
 About: Results were produced by the GenCore software, version 4.5,
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/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-997-803-13	1	854.50	1760.91	2.0e-90	1356
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-997-803-12	1	850.50	1751.02	7.0e-90	1523
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/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-997-803-3	1	589.50	1212.77	6.7e-60	639
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-196-989B-3	1	539.50	1091.69	3.7e-53	2232
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-760-936-3	1	539.50	1091.69	3.7e-53	2232
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-09-087-888-1	1	499.50	1016.06	6.0e-49	1137
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/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-706-281A-17	1	327.00	654.95	7.9e-29	978
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-097-231-17	1	327.00	654.95	7.9e-29	978
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-671-525B-9	1	326.00	652.88	1.0e-28	975
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-672-109B-9	1	326.00	652.88	1.0e-28	975
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/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-842-238-9	1	326.00	652.88	1.0e-28	975
/cgn2_6/ptodata/2/ina/6A.COMB.seq:US-08-842-238-9	1	326.00	652.88	1.0e-28	975
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seq documentation block:
; Sequence 1, Application US/08861747
; Patent No. 6020158
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: VYAS, Tejal B.
; TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 15th St., NW, Suite 330 - G Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,747
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jahns, Kristina M.
; REGISTRATION NUMBER: 41,092
; REFERENCE/DOCKET NUMBER: P8074-7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1761 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-861-747-1

alignment_scores:
  Quality: 1941.00 Length: 383
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34 alValValAlaLeuGlyLeuThrValSerValLeuValLeuThrAsn 50
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alignment_scores:
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527  GTCCGTGGCCACACTGCTGGCCATCGCGTGGACGGACCGCAGTGTGA 576
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151  ileValGlyValTrpValAlaAlaLeuGlyLeuGlyLeuLeuProAlaHi 167
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167  sSerTrpHisCysLeuCysAlaLeuAspArgCysSerArgMetAlaProL 184
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184  euLeuSerArgSerTyrLeuAlaValTrpAlaLeuSerSerLeuLeuVal 200
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201  PheLeuLeuMetValAlaValTyrThrArgIlePhePheTyrValArgAr 217
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seq_documentation_block:
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Patent No. 6037146
GENERAL INFORMATION:
APPLICANT: Sathe, Ganesh
APPLICANT: Bergsma, Derk
TITLE OF INVENTION: CDNA CLONE HE8CH90 THAT ENCODES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/789,982
FILING DATE: 28-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: ATG50050
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1260 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-789-982-1
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Quality: 1914.00 Length: 376
Ratio: 5.104 Gaps: 1
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alignment_block:
US-09-274-752d-1 x US-08-789-982-1
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; Patent No. 5998164
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR2
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION NUMBER: US/08/467,948A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2185 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 884..2062
; US-08-467-948A-3

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; Quality: 1484.50      Length: 359
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174 IaLeuAspArgCysSerArgMetAlaProLeuLeuSerArgSerTyrLeu 190
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Ratio: 3.357 Gaps: 8

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1860 CACTATACATCTCTGCCAGGAGGTGCCAGCACTCGCATCATGCTTCC 1909
340 oGluAsnGlyHisProLeuMet.ThrProProPheSerTyrLeuGluLeu 356
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1910 CGAGAACGGCCACCCACTGATGACTCCACCCCTTAGCTACCTTGAAC 1959
357 GlnArgTyrAlaAlaSerAsnLysSerThrAlaProAspAspLeuTrpVa 373
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seq_name: /cgn2_6/ptodata/2/lna/6A_COMB.seq:US-08-763-938-1
seq_documentation_block:
: Sequence 1, Application US/08763938
: Patent No. 6140060
: GENERAL INFORMATION:
: APPLICANT: CHUN, Jerold J.M.
: APPLICANT: HECHT, Jonathan H.
: TITLE OF INVENTION: CLONED LYOPHOSPHATIDIC ACID
: NUMBER OF INVENTION: RECEPTORS
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP
: STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-5701
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/763,938
: FILING DATE: 12-DEC-1996
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: JAHNS, Kristina M.
: REGISTRATION NUMBER: 41,092
: REFERENCE/DOCKET NUMBER: P8074-6018
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 638-5000
: TELEFAX: (202) 638-4810
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2250 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-763-938-1
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Align seg 1/1 to: US-08-763-938-1 from: 1 to: 2250

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39  lyLeuThrValSerValLeuValLeuLeuThrAsnLeuLeuValIleAla 55
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56  AlaIleAlaSerAsnArgArgPheHisGlnProIleTyrTyrLeuLeuG1 72
444 GCAATCTACCTCAACCGCCGCTTCCATTTCCCTATTATTACTTGATGGC 493
72  yAsnLeuAlaAlaAlaAspLeuPheAlaGlyValAlaTyrLeuPheLeuM 89
494 CAACCTGGCTGCTGCAGACTTCTCGCTGGATGGCTACTTCTACCTGA 543
89  etPheHisThrGlyProArgThrAlaArgLeuSerLeuGluGlyTrpPhe 105
544 TGTTCAATCAGGACCTTAATACCGGAGACTGACTGTTAGCACCTGCTC 593
106  LeuArgGlnGlyLeuLeuAspThrSerLeuThrAlaSerValAlaThrLe 122
594 CTCGGCAGGGCTCATTTGACACAGCCTGACAGCTTCTGTGGCCAACT 643
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139  isSerArgLeuProArgGlyArgValValMetLeuIleValGlyValTrp 155
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744 ACTATGGCCATTGTGATGGTGTGTATACCCAGCTGGGCTGGAACTGCAT 793
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794 CTGTGATATCGATCACTGTTCACATGGCACCCCTCTACAGTGACTCCT 843
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844 ACTTACTCTCTGGGCCATTTTCAACCTGGTGACCTTTGTGGTGGTGGT 893
206  AlaValTyrThrArgIlePhePheTyrValArgArgValGlnArgMe 222
894 GTTCTCTAGCTCACATCTTTGGCTATGTTGGCCAGAGGACTATGAGGAT 943
222  tAlaGluHisValSerCysHisProArgTyrArgGluThrThrLeuSerL 239
944 GTCTCGCATAGTCTTGGACCCAGGAGGAATCGGACACCATGATGAGCC 993
239  euVallyThrValValIleIleLeuGlyAlaPheValValCysTrpThr 255
994 TTTGAAGACTGTGGTCAATGTGCTGGTGGCTTTTATTGTCTGCTGGCAT 1043
256  ProGlyGlnValValLeuLeuAspGlyLeuGlyCysGluSerCysAs 272
1044 CCGGGATTGGCTGTGTTATGCTGGAT...GTGTGCTGCCCGGAGTGGCA 1090
272  nValLeuAlaValGluGlyTyrPheLeuLeuLeuAlaGluAlaAsnSerL 289
1091 TGTCTCTGGCCTATGAGAAGTCTTCTCTCTCTCTCTCTCTCTCTCTCT 1140
289  euValAsnAlaAlaValTyrSerCysArgAspSerGluMetArgThr 305
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1141 CTATGAACCCCATCATCTACTCTCTACCGCAGCAAAAGAGATGAGCGCCACC 1190
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1191 TTCAGGCAGATCCTGTGTGC.....CAGCGCAACGAGA..... 1224
322  ervAlHisTyrThrSerSerAlaGlnGlyGlyAlaSerThrArgIleMet 338
1225 .....ACCTAATGGCCCGCCAGGAGCTCTGACC.....GCT 1257
339  LeuProGluAsnGlyHisProLeuMetThrProPheSerTyrLeuG1 355
1258 CTGCT.....CCTCCCTCAACACCATTC...TGCGTGA 1292
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seq_documentation_block:
Sequence 1, Application PC/TUS9610618
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Guegler, Karl J.
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10618
FILING DATE: 20-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,352
FILING DATE: 20-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/567,817
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: PF-0042 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1875 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Rheumatoid Synovium
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CLONE: 80853
PCT-US96-10618-1

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425 GCATCTTGGCCACAGATGGAACAGTCAGCAAGCTGGTGGACITG 474
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475 GAATCACTGTTGTATCTTCTATCATGTGTGGCCAACTATTGTCATGGTG 524
56 AlaIleAlaSerAsnArgArgPheHisGlnProIleTyrTyrLeuGlu 72
525 GCAATCTATGTCACCGCGCTTCCATTTCTTATTTATTAACCTAATGGC 574
72 yAsnLeuAlaAlaAlaAspLeuPheAlaGlyValAlaTyrLeuPheLeu 89
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89 etPheHisThrGlyProArgThrAlaArgLeuSerLeuGluGlyTrpPhe 105
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106 LeuArgGlnGlyLeuLeuAspThrSerLeuThrAlaSerValAlaThrLe 122
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq.us-08-997-803-13
seq_documentation_block:
; Sequence 13, Application US/08997803
; Patent No. 6057126
; GENERAL INFORMATION:
; APPLICANT: CHUN, Jerold J.M.
; APPLICANT: GUPTA, Ashwani
; APPLICANT: MUNROE, Donald G.
; APPLICANT: VIAS, Tejal B.
; TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth Street, N.W., Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/997,803
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wong, King L.
; REGISTRATION NUMBER: 37,500
; REFERENCE/DOCKET NUMBER: P8074-7020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1356 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-997-803-13

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Quality: 854.50 Length: 386
Ratio: 3.052 Gaps: 5
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US-09-274-752D-1 x US-08-997-803-13

Align seg 1/1 to: US-08-997-803-13 from: 1 to: 1356

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69 rLeuLeuGlyAsnLeuAlaAlaAspLeuPheAlaGlyValAlaTyrL 86
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586 GCAGGAGTTACCTTGTCTTGACAGCTGTCCAACCTCATGGCCTCTC 635
203 LeuMetValAlaValTyrThrArgIlePhePheTyrValArgArgVa 219
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seq_documentation_block:
Sequence 12, Application US/08997803
Patent No. 6057126
GENERAL INFORMATION:
APPLICANT: CHUN, Jerold J.M.
APPLICANT: GUPTA, Ashwani
APPLICANT: MUNROE, Donald G.
APPLICANT: VYAS, Tejal B.
TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street, N.W., Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,803
FILING DATE: 24-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wong, King L.
REGISTRATION NUMBER: 37,500
REFERENCE/DOCKET NUMBER: P8074-7020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1523 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 261..1322
US-08-997-803-12

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alignment_block:
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20 rGlyLysGluLeuSerSerHisrPArg...ProLysaspValValValv 36
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86 euPheLeuMetPheHisThrGlyProArgThrAlaArgLeuSerLeuGlu 102
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119 lAlaThrLeuLeuAlaIleAlaValGluArgHisArgSerValMetAlav 136
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611 CACCAACTTCTGTTATTCGCGGTGAGAGGCACATGTCATCATAGGA 660
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
136 alGlnLeuHisSerArgLeuProArgGlyArgValValMetLeuVal 152
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
661 TGGCGGTCCATAGCAACCTGACCAAAAGAGGGTGACACTGCTCATTTG 710
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
153 GlyValTrpValAlaLeuGlyLeuGlyLeuLeuProAlaHisSerTr 169
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
711 CTGTCTGGCCATCGCCATTTTATGGGGCGGTCCCCACACTGGGGCTG 760
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
169 pHisCysLeuCysAlaLeuaspArgCysSerArgMetAlaProLeuLeuS 186
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
761 GAATTCCTCTGCAACATCTCTGCTGCTCTCTCCCTGGCCCATTTTACA 810
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
186 erArgSerTyrLeuAlaValTrpAlaLeuSerSerLeuValPheLeu 202
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
811 GCAGGAGTTACCTTGTCTTGGACAGTGTCCAACTCATGCGCTTCCTC 860
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
203 LeuMetValAlaValTyrThrArgIlePhePheTyrValArgArgVa 219
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861 ATCATGTTGTGGTGTACCTGCGGATCTACGTGTACGTCAAGAGGAAAC 910
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219 lGlnArgMetAlaGluHisValSerCysHisProArgTyrArgGluThrT 236
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911 CAACGCTTCTCTCCGATCAACAGTGGTCCATCAGCCCGCGGAGGACAC 960
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236 hrLeuSerLeuValLysThrValValIleLeuGlyAlaPheValVal 252
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253 CysrPrpThrProGlyGlnValValLeuLeuLeuAspGlyLeuGlyCysG 269
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seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-325-897-1

seq_documentation_block:
; Sequence 1, Application US/09325897
; Patent No. 6242572
; GENERAL INFORMATION:
; APPLICANT: Ping Tsui
; APPLICANT: Catherine E. Ellis
; APPLICANT: Ganesh M. Sathe
; APPLICANT: Stephanie Van Horn
; APPLICANT: Robert S. Ames
; APPLICANT: James J. Foley
; APPLICANT: Laura R. Fitzgerald
; APPLICANT: Harry M. Sarau
; APPLICANT: Jonathon K. Chambers
; TITLE OF INVENTION: HUMAN G PROTEIN COUPLED RECEPTOR
; FILE REFERENCE: GH70014-2
; CURRENT APPLICATION NUMBER: US/09/325,897
; EARLIER FILING DATE: 1999-06-04
; EARLIER APPLICATION NUMBER: 09/215,072
; EARLIER FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 08/992,031
; EARLIER FILING DATE: 1997-12-17
; EARLIER APPLICATION NUMBER: 60/046,366
; EARLIER FILING DATE: 1997-05-13
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1065
; TYPE: DNA
; ORGANISM: Human
; US-09-325-897-1

alignment_scores:
  Quality: 849.00      Length: 346
  Ratio: 3.216         Gaps: 2
  Percent Similarity: 76.301  Percent Identity: 46.821

alignment_block:
US-09-274-752D-1 x US-09-325-897-1 ..

Align seg 1/1 to: US-09-325-897-1 from: 1 to: 1065

4 MetGlyClnCysTyrTyrAsnGluThrIleGlyPhePheTyrAsnAsnSe 20
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
1 ATGAATGAGTGTCACTATGACAAACACATGACATGCTTTTATATAGGAG 50
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91 HisThrGlyProArgThrAlaArgLeuSerLeuGlyTyrPheLeuAr 107
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1 AACACTGGCCCGGTGTCGAAACAGTTGACCGCTCAACCCCTGGTCTCTCG 50

107 gCInGlyLeuLeuAspThrSerLeuThrAlaSerValAlaThrLeuA 124
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51 CCAGGGGTCTTAGACACCAGCCTGACTGCTTCCTCGCTGCAATTGGTGG 100
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124 laileAlaValGluArgHisArgSerValMetAlaValGlnLeuHisSer 140
101 TTATTGCTGGAAGACACATGTCNATCATGAGGATGAGATCCACAGC 150
141 ArgLeuProArgGlyArgValValMetLeuLeuValGlyValTrpValAl 157
151 AACTTGACCAAAAGCGGTGACGCTGCTATTCTGCTGCTGGGCAT 200
157 aAlaLeuGlyLeuLeuLeuProAlaHisSerTrpHisCysLeuCysA 174
201 CGCATCTTTCATGGGGCGGCGCCACACNCTGGGATGGAATGCCCTGCA 250
174 laLeuAspArgCysSerArgMetAlaProLeuLeuSerArgSerTyrLeu 190
251 ACATCTGGCCTGCTCTCTGCTGCTCCATTTACAGTAGGAGTACCTC 300
191 AlaValTrpAlaLeuSerSerLeuValPheLeuLeuMetValAlaVal 207
301 ATTTTCTGGAGCTGTCTCAACCTCTGCTGCTTCTTCATCATGCTGGCGGT 350
207 lTyrThrArgIlePhePheTyrValArgArgValGlnArgMetAlaG 224
351 ATACGTACGCATCTACATGTATGTATAAGGAAACCAACGCTTTATCTC 400
224 luHisValSerCysHisProArgTyrArgGluThrThrLeuSerLeuVal 240
401 CACACACAGCTGGCTCCATCAGCCCGGAGGGCTCCCATGAGTAATG 450
241 LysThrValValIleIleLeuGlyAlaPheValValCysTrpThrProG 257
451 AAGACAGTGATGACCGCTTAGGCGCTTCTGCTGCTGCTGAGCCCGG 500
257 yGlnValValLeuLeuLeuAspGlyLeuGlyCysGluSerCysAsnVal 274
501 TCTGTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 550
274 euAlaValGluLysTyrPheLeuLeuLeuAlaGluAlaAsnSerLeuVal 290
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291 AsnAlaAlaValTyrSerCysArg 298
601 AACCCCTCATCTAC...TGCCGC 621

seq_name: /cgn2_5/ptodata/2/ina/5A_COMB.seq:US-08-196-989B-3

seq_documentation_block:
; Sequence 3, Application US/08196989B
; Patent No. 5585476
; "GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,989B
; FILING DATE: 15-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff

REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MAC-100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2232 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 269..1420
US-08-196-989B-3

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Quality: 539.50 Length: 308
Ratio: 2.581 Gaps: 6
Percent Similarity: 67.857 Percent Identity: 37.987
alignment_block:
US-09-274-752D-1 x US-08-196-989B-3
Align seg 1/1 to: US-08-196-989B-3 from: 1 to: 2232

17 TyrAsnAsnSerGlyLys.....GluLeuSerSerHisTr 28
356 TACAACATACACAGCAAGCTAACATCGGAGTGGAGAGGACCATGGCAT 405
28 pargProLysAspValValValAlaLeuGlyLeuThrValSerValL 45
406 TAAACTGACTTCAGTGGTGTTCATT.....CTCATCTGCTGCT 443
45 euValLeuLeuThrAsnLeuValIleAlaIleAlaSerAsnArg 61
444 TCATCATCTAGAGATATATTGCTTCTTAACCTATTGGAAACCAAG 493
62 ArgPheHisGlnProIleTyrLeuLeuGlyAsnLeuAlaAlaAs 78
494 AAGTTCCACCGCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 543
78 pleuPheAlaGlyValAlaTyrLeuPheLeuMetPheHisThrGlyProA 95
544 CCGTGTAGCAGGAGTGGCTTACACAGCTAACCTGCTGTTCTGTGGGCCA 593
95 rgThrAlaArgLeuSerLeuGluGlyTyrPheLeuArgGlnGlyLeuLeu 111
594 CCACCTACAGCTCACACCTGCCAGTGGTTCTGCGGGAAGGAGTATG 643
112 AspThrSerLeuThrAlaSerValAlaThrLeuLeuAlaIleAlaValG 128
644 TTTGTGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 693
128 uArgHisArgSerValMetAlaValGlnLeuHisSerArgLeuProArg 145
694 GCGCTACATCACCATGCTGAAGATGAACCTACACAACGCGCACAGCT 743
145 lyArgValValMetLeuIleValGlyValTrpValAlaAlaLeuGlyLeu 161
744 CGCGCTCCTTTCTGCTGATCAGTGGCTGCTGCTGCTGCTGCTGCTGCTG 793
162 GlyLeuLeuProAlaHisSerTrpHisCysLeuCysAlaLeuAspArgCy 178
794 GCTGGGCTGCCCATCATGCTGGCTGGAACTCATCAGCTGCTGCTGCTG 843
178 sSerArgMetAlaProLeuLeuSerArgSerTyrLeuAlaValTrpAlaL 195
844 CTCACCGCTGCTCCCGCTCTACCAACAGCACTATATTCTTCTGACCA 893
195 euSerSerLeuLeuValPheLeuLeuMetValAlaValTyrThrArgIle 211

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17  TyrAsnAsnSerGlyLys.....GluLeuSerSerHisTrp 28
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28  pargProLysAspValValValAlaLeuGlyLeuThrValSerVal 45
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406 TAAACCTAGCTTCAGTGGTGTTCATT.....CTCATCTCTGCTGT 443
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45  euValLeuLeuThrAsnLeuLeuValLleAlaAlaLeuAlaSerAsnArg 61
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444 TGATCATCTCTAGAGAATATATTGCTTGCCTAACTATTGGAAACCAAC 493
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62  ArgPheHisGlnProLeyTyrLeuLeuGlyAsnLeuAlaAlaAs 78
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494 AAGTTCACCGGCCCATGTACTATTTCATAGGCAACCTAGCCCTCTCG 543
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78  PhePheAlaGlyValAlaTyrLeuPheLeuMetPheHisThrGlyPro 95
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544 CCGTGTACAGAGTGGCTTACACAGCTAAACCTGCTGTGTCTGGGGCCA 593
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95  rgThrAlaArgLeuSerLeuGluGlyTyrPheLeuArgGlnGlyLeu 111
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794 GGTGGGCTGCCATCATGGCTGGAAGTGCATCAGCTCGCTGTCCAGCT 843
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178 sSerArgMetAlaProLeuLeuSerArgSerTyrLeuAlaValTyrAl 195
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212 PhePheTyrValArgArgValGlnArgMetAla.....GluHisVa 226
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226 lserCysHisProArgTyrArgGluThrThrLeuSerLeuValLysThr 243
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994 CTCCAAGGCCAGCCGCACTTCCGAGAAGTCTCTGCGCTTGTGAAGAC 1043
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243 alValLleLeuGlyAlaPheValValCysTrpThrProGlyGlnVal 259
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; NAME/KEY: CDS

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335 hrArgIleMetLeuProGluAsnGlyHisProLeuMetThrProPhe 351
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977 CACCCATC.....CAGCCTGGCTCGACCCCAAGCAGA 1008

352 SerTyrLeuGluLeuGlnArgTyrAlaAlaSerAsnLysSerThrAlaPr 368
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-196-989B-1

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seq_documentation_block:
; Sequence 1, Application US/08196989B
; Patent No. 5585476
; GENERAL INFORMATION:
; APPLICANT: MacLennan, A. John
; TITLE OF INVENTION: Molecular Cloning and Expression of
; TITLE OF INVENTION: G-Protein Coupled Receptors
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: US
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/196,989B
; FILING DATE: 15-FEB-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Lloyd, Jeff
; REGISTRATION NUMBER: 35,589
; REFERENCE/DOCKET NUMBER: MAC-100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2754 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-196-989B-1

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 Ratio: 2.223 Gaps: 10
 Percent Similarity: 62.396 Percent Identity: 35.933

alignment_block:

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23 uLeuSerSerHisTTrpArgProLysAspValValValValValAlaLeuGlyL 40
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
219 GCTGACATGACGAGAGACGCTCCCGCAAGGTGGCCTCCGCTTCATCA 268

40 euThrValSerValLeuValLeuLeuThrAsnLeuLeuValIleAlaAla 56
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57 IleAlaSerAsnArgArgPheHisGlnProIleTyrTyrLeuLeuGlyAs 73
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73 nLeuAlaAlaAspLeuPheAlaGlyValAlaTyrLeuPheLeuMetP 90
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369 CTGGCAGCCTCCGACCTGCTGGCAGCGGTGGCCTTCGTGGCCAAACACT 418

90 heHisThrGlyProArgThrAlaArgLeuSerLeuGluGlyTrpPheLeu 106
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
419 TGCTCTCGGACCTGTACCTGTCTTAACCTCCCTTGCAGTGGTTGCC 468

107 ArgGlnGlyLeuLeuAspThrSerLeuThrAlaSerValAlaThrLeuLe 123
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469 CGAGAGGTTGAGCCTTCATCAGCGTCTCTGCTCGTCTTCAGCCTCCT 518

123 uAlaIleAlaValGluArgHisArgSerValMetAlaValGlnLeuHis 140
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173 sAlaLeuAspArgCysSerArgMetAlaProLeuLeuSerArgSerTyrL 190
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719 TGCTCTGCTGTGTCACCATCTCTCTGCTCATCTTACTGGCTATCTGGGC 768

207 ValTyrThrArgIlePhePheTyrValArgArgValGlnArgMetAl 223
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
769 TTGTACGTCGGAATCTACTTCGTAGTCCGC.....TC 800

223 aGluHisValSer....CysHisProArgTyrArgGluThrThrLeuSerL 239
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801 AAGCCATCGGACGCTGCTGGTGGCTCAG.....ACGCTGGCCC 838

239 euValLysThrValValIleIleLeuGlyAlaPheValValCysTrpThr 255
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839 TGCTCAAGACAGTCACCATCGTGGGTGTTTTCATCATCTGCTGGGTG 888

256 ProGlyGlnValValLeuLeuAspGlyLeuGlyCys.....GluSe 270
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270 rCysAsnValLeuAlaValGluLysTyrPheLeuLeuLeuAlaAla 287
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936 CTGTCTCTCTCTACAAAAGCCCATTTCTTCTTCTTCTTCTTCTTCTTCT 985

287 snSerLeuValAsnAlaValTyrSerCysArgAspSerGluMetArg 303
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304 ArgThrPheArgLeuLeuCysCysAlaCysLeuArgGlnSerThrAr 320
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1036 AGGAGGTACTAGGCCCTG.....CTGTCTGGCGGCAGGGGAAGGG 1079
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1080 A.....GCACAGGCGCGAGAGGTGGAAACCCGTGTCACC 1114
337 leMetLeuPro.....GluAsnGlyHisProLeu 346
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347 MetThrProProPheSerTyrLeuGlu 355
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4	860.4	49.6	2185	2	US-08-467-948A-3	Sequence 3, Appli
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6	364	21.0	2250	3	US-08-763-938-1	Sequence 1, Appli
7	324.4	18.7	1875	5	PCT-US96-10618-1	Sequence 1, Appli
8	282	16.3	1065	4	US-09-325-897-1	Sequence 1, Appli
9	279.6	16.1	1356	3	US-08-997-803-13	Sequence 13, Appl
10	278	16.0	1523	3	US-08-997-803-12	Sequence 12, Appl
11	181.8	10.5	639	3	US-08-997-803-3	Sequence 3, Appli
12	180.4	10.4	1637	3	US-08-852-824-3	Sequence 3, Appli
13	163.2	9.4	2232	1	US-08-196-989B-3	Sequence 3, Appli
14	163.2	9.4	2232	2	US-08-760-936-3	Sequence 3, Appli
15	161.4	9.3	1649	2	US-08-845-566-2	Sequence 2, Appli
16	128.4	7.4	1137	3	US-09-082-088-1	Sequence 1, Appli
17	120.2	6.9	2754	1	US-08-196-989B-1	Sequence 1, Appli
18	120.2	6.9	2754	2	US-08-760-936-1	Sequence 1, Appli
19	62.8	3.6	1776	1	US-08-722-001-29	Sequence 29, Appl
20	61.2	3.5	1621	1	US-08-722-001-13	Sequence 13, Appl
21	61.2	3.5	2140	1	US-08-334-698-1	Sequence 1, Appli
22	61.2	3.5	2140	1	US-08-228-932-1	Sequence 1, Appli
23	61.2	3.5	2140	1	US-08-468-939-1	Sequence 1, Appli
24	61.2	3.5	2140	2	US-08-406-855A-1	Sequence 1, Appli
25	61.2	3.5	2140	2	US-08-722-190-1	Sequence 1, Appli
26	61.2	3.5	2140	3	US-08-244-354-1	Sequence 1, Appli
27	61.2	3.5	2140	3	US-09-206-899-1	Sequence 1, Appli

Qy	62	ctgcggcgtgaactgagagcccaagatggtcatcatatgggccagtgctactacaacagacacca	121
Db	68	ctgcggcgtgaactgagagcccaagatggtcatcatatgggccagtgctactacaacagacacca	127
Qy	122	tcggctctcttcataacaacagtggtcaaaagagctcagctcccactggtgcggccaaagatg	181
Db	128	tcggctctcttcataacaacagtggtcaaaagagctcagctcccactggtgcggccaaagatg	187
Qy	182	tggctgtgtgtgcaactggggtgacccgtcagcgtgctgtggtgtgctgtgaccaaattcgtcg	241
Db	188	tggctgtgtgtgcaactggggtgacccgtcagcgtgctgtggtgtgctgtgaccaaattcgtcg	247
Qy	242	tcaatagacacatcgccctccaaacccgcgcttcacacagcccatctactactcgtcgtcgga	301
Db	248	tcataagacacatcgccctccaaacccgcgcttcacacagcccatctactactcgtcgtcgga	307
Qy	302	atctgcgcggcgtgacacctcttcgcggcgtgtggctacctcttctcatgtttccacaactg	361
Db	308	atctgcgcggcgtgacacctcttcgcggcgtgtggctacctcttctcatgtttccacaactg	367
Qy	362	gtcccgacacagcccgactttcaacttgagggtgctggttctcgtgcgcaggggtctctggaca	421
Db	368	gtcccgacacagcccgactttcaacttgagggtgctggttctcgtgcgcaggggtctctggaca	427
Qy	422	caagcctcactgcgtggtgtggccacactgctgtggccatcgcgtagagctgcacccgagtg	481
Db	428	caagcctcactgcgtggtgtggccacactgctgtggccatcgcgtagagctgcacccgagtg	487
Qy	482	tgatgtccgtcagctgcacagccgcttgcacctgcccgtggtgcgcgctggtcatctcatgttg	541
Db	488	tgatgtccgtcagctgcacagccgcttgcacctgcccgtggtgcgcgctggtcatctcatgttg	547
Qy	542	gcgtgtgggtggctgcctggcctggggtgctgctgctgcccactccttgcaactgcctct	601
Db	548	gcgtgtgggtggctgcctggcctggggtgctgctgctgcccactccttgcaactgcctct	607
Qy	602	gtgccttgacccgtgctcaacgcatggcacccctgctcagcgcgctcctattttggcgcgtct	661
Db	608	gtgccttgacccgtgctcaacgcatggcacccctgctcagcgcgctcctattttggcgcgtct	667
Qy	662	gggctgtgtcagcctgtctcttcctgctcatgtgtgctgtatcacccgattttct	721
Db	668	gggctgtgtcagcctgtctcttcctgctcatgtgtgctgtatcacccgattttct	727
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Db	728	tatatcgtgcggcggcagtgacgcgcgatggcagagcatgtcagctgccaaccccgctacc	787
Qy	782	gagacacacgctcagccttggctcagactgttbtteatcctctggggcgttcgtgtgctct	841
Db	788	gagacacacgctcagccttggctcagactgttbtteatcctctggggcgttcgtgtgctct	847
Qy	842	gctggacacacggtcaggttggctacgtcctctgtagtgttttaggctgtgagtccttgcgaatg	901
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Qy	902	tcctggcgttagaaaaagtacttctcactgttggccgagggccaaactcactggtcgaatgctg	961
Db	908	tcctggcgttagaaaaagtacttctcactgttggccgagggccaaactcactggtcgaatgctg	967
Qy	962	ctgtgtactcttgcgagatgctgagatgcgcgcgcacacctccgcgcctctctctgtgcg	1021
Db	968	ctgtgtgtactcttgcgagatgctgagatgcgcgcgcacacctccgcgcctctctctgtgcg	1027
Qy	1022	cgtgtcctccgcaggtccacccgcgagctgtgtccactatacatctctctgcccagggaggtg	1081
Db	1028	cgtgtcctccgcaggtccacccgcgagctgtgtccactatacatctctctgcccagggaggtg	1087
Qy	1082	ccagcactcgcatactgtctcccgagaacggccacccactgat-gactccacccctttagc	1140
Db	1088	ccagcactcgcatactgtctcccgagaacggccacccactgat-gactccacccctttagc	1147
Qy	1141	tacctgtgaactctcagcggtaacygcgcgaagaacaataaccacagcccttgtagctgttg	1201

Db	1148	TACCTTGAATCTCAGCGGTACCGCGCAGACAAACAATCCACAGCCCTGATGACTTGTGG	1207
Qy	1201	gtgctccttgctcaaccacacacacagactgactgctgcagagcaaatgcttggcatg	1260
Db	1208	GTGCTCTCGTCAACCCAAACACAGGACTGACTGACCGCGCAGGACAAAGGTCTGGCATG	1267
Qy	1261	gcacagcaccactgccaggcctcccccagcgacacacacactctgccccaggggaatgggggcttt	1320
Db	1268	GCACAGCACACTGCCAGGCCCTCCCGACGCACACACACTCTGCCAGGGAATGGGGGCTTT	1327
Qy	1321	gggtcatctcccactgctcggggsgtgcagatggsgtgcaggaatctggctcttcacgcca	1380
Db	1328	GGGTCACTCCCACTGCTCTGGGGAGTCAGATGGGTGCAGGAATCTGGCTCTTCAGCCA	1387
Qy	1381	tctcaggttttagggggtttgtatacagacattattctgttttcaactgcgtatccttgtaa	1440
Db	1388	TCOCAGGTTTAGGGGTTTGTTAACAGACATTATTCTGTTTTCACTGGGTATCCTTGTGTA	1447
Qy	1441	gcctctgactgggttaatgctgtgtatctgactgagggttttaagctgggaagagataagg	1500
Db	1448	GCCTGTGGACTGGTTCCTTCGCTGTGTGATCTGAGGGTTTAAAGTGGGAGAGATAAGG	1507
Qy	1501	gctctctcgggccatgctaccgggtatgactgggttaatgagacagactgtggacacccc	1560
Db	1508	GCCTCTCGGGCCATGCTACCCGGTATGACTGGGTAATGAGGACAGACTGTGGACACCCC	1567
Qy	1551	atctactgagtctgattcttttagcagcagactgaggggtgcagagctgtaagctggga	1620
Db	1558	ATTACTGAGTCTGATTCTTTAGCAGCAGAGACTGAGGGGTGCAGAGTGTGAGCTGGGA	1627
Qy	1621	aaggtttggtcccttgctcagctccacggagctgccttgcctcccaatagaattgaagcag	1680
Db	1628	AAGGTTTGTGGCTTCCTTTCAGAGCTCCAGGGACTGGCCCTGTCCCGATAGAAATTGAACG	1687
Qy	1681	tcacagggaggggatgatcacagagagtaaacctttctttacactc	1726
Db	1688	TCACGGGAGGGGATGATACAGAGAGTAAACCTTCTTTTACACTC	1733

RESULT

US-08-861-747-3
Sequence 3, Application US/08861747
Patent No. 6020158
GENERAL INFORMATION:
APPLICANT: MUNROE, Donald G.
APPLICANT: VYAS, Tejal B.
TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaído, Marmelstein, Murray & Oram LLP
STREET: 655 15th St., NW, Suite 330 - G Street Lobby
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/861,747
FILING DATE: 22-MAY-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Jahus, Kristina M.
REGISTRATION NUMBER: 41,092
REFERENCE/DOCKET NUMBER: P8074-7003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 3:

;	SEQUENCE CHARACTERISTICS:									
;	LENGTH: 1889 base pairs									
;	TYPE: nucleic acid									
;	STRANDEDNESS: single									
;	TOPOLOGY: linear									
;	MOLECULE TYPE: cDNA									
US-08-861-747-3										
	Query Match	96.9%	Score 1680;	DB 3;	Length 1889;					
	Best Local Similarity	98.7%;	Pred. No. 0;							
	Matches 1703;	Conservative	1;	Mismatches	21;	Indels	1;	Gaps		
Qy	2	gcaagagcgccggggccatgggctcgagccgcccgcgcgaacccccgcagccccgcagccccgttgt	61							
Db	94	GCACAGCTCGCCGGCCATGGGCTCGAGCGCCGCCCGAACCACCCCGCGAGCCGCCCTGT	153							
C	62	ctgcggcgctgactggaggcccaatggtcatcatgctggccagtcgtactactacaaagagacca	121							
Db	154	CTGGCGCGTCACTGGAGGCCCAATGGTCAATATGGCCAGTGTCTACTACAAGAGACCA	213							
Qy	122	tcggctctctctataacaaacagctggcaagagctcagctcccactggcgcccaagatg	181							
Db	214	TCGGTTTCTTCTATAACAACAGTGGCAAGAGCTCAGCTCCCACTGGCGGCCCAAGATG	273							
Qy	182	tggctggtgggaactggggctgacggtcagcgtgctggtgctgctgacaaatctgctgg	241							
Db	274	TGGTCTGTGGTGGCACTGGGGCTGACCGTCAAGCGTGTGTGTCTGTCTGTGACCAATCTCTGTGG	333							
Qy	242	tcatagcagcatctgcctccaaacgcgcgtctcaacagcccatctactacctgctcgcca	301							
Db	334	TCATAGCAGCATGCGCTCCACCGCGCTTCCACAGCCCATCTACTACCTGCTCGGCA	393							
Qy	302	atctggcgcggctgacctctctcgggggcggtcgctacacctctctctcatgttccacagt	361							
Db	394	ATCTGGCCGCGGTGACCTCTTTCGGGGCGCTGGCCCTACCTCTTCTCATGTTCACACTG	453							
Qy	362	gtccccgcacagcccgacttctcaactgagggctggttctctgcggcgaggctgctggaca	421							
Db	454	GTCCCCGCACAGCCCGACTTTCATCTTGAGGGCTGGTTCCTTGGCGCAGGGCTGTCTGGACA	513							
Qy	422	caagcctcactgcgtcggtggccacactcgtgcccatcgccgtgagctgaccccgagtg	481							
Db	514	CAAGCCTCACTGCTGCGTGGCGCCACACTGCTGGCCATCGCCGTGGAAACGGCACCGCAGTG	573							
C	482	tgatctcgctgacgtcacagccgcctgcccgtggcggtggctcatgctcattgtgg	541							
Db	574	TGATGGCCGTACAGTTGCACAGCGCCTGCCCGTGGCCGCGTGCATGCTCATTTGTGG	633							
Qy	542	gcgtgtgggtggtgccttgggctggggctgctgctgctgcccactccttggcactgcctct	601							
Db	634	GCFTGTGGGTGGTGGCCCTGGGGCTTGGGGCTGGTGGCTGGCCACTCTCTGGCACTGGCTCT	693							
Qy	602	gtgccctggaccgctgctcacgcatggcacccctgctcacgcccctcctatttggcgctct	661							
Db	694	GTGCCCTTGGACCGCTGTCTACAGATGGCACCCCTGTCTACGCCCTCTATTGGCCGCTG	753							
Qy	662	gggctctgtgcagcctgtctgtcttctcgtcatgttggtgctgtgtacaccccgcatttct	721							
Db	754	GGGCTCTGTGAGCCTGCTTGTCTTCTGTGCTCATGTGTGGGTGTGTACACCCGCATTTTTT	813							
Qy	722	tctacgtgcggcgagtcagcgcatggcagagcatgtcaactgccacccccgcgtacc	781							
Db	814	TATACGTGTGGCGCGAGTGCAGCGCATGGCAGAGATGTCAGCTGCCACCCCGGTACG	873							
Qy	782	gagagaccacgctagcctgggtcaagactgtgtcatcatctctctggggcggttcgtggct	841							
Db	874	GAGAGACCAGCCTCAGCCTGGTCAAGACTGTTGTTCATCTCTTGGGGCGCTGCTGGTCT	933							
Qy	842	gctggacaccagggctggtactgctcctgatatggtttaggtgtgagtcctgcaatg	901							
Db	934	GCTGGACACAGGCCAGGTGGTACTGTCTCTGGATGTTTGTAGCTGTGAGTCTCTGCAATG	993							

; STATE: PA

; STATE: PA

ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 884..2062
US-08-467-947A-3

Query Match. 49.6%; Score 860.4; DB 2; Length 2185;
Best Local Similarity 97.9%; Pred. No. 2.3e-202;
Matches 914; Conservative 0; Mismatches 16; Indels 4; Gaps 4;

Qy 292 ctgctcggaatctggcggcggtgacct-cttcggggggtggcctacctctctctcat 350
Db 1097 CTCGCGCAATCTCTCGCGGCTGACCTCTTCGCGGCGTGGCTACCTCTCTCTCAT 1156
Qy 351 gttcacactggtcccgacacgacgactttcaacttgaggctggtctcgccaggg 410
Db 1157 GTTCCACACT-GTCCCCGACACGCCGACTTTTCACTTGAGGGGTGTTCTCGCGGAGG 1215
Qy 411 cttgtgacacaaagcctcactgctggtgacacactggtggcctgcgctgagct 470
Db 1216 CTGTGTGACACAAACCTCCTACGCTGCGTGGTGCCACACTGCTGGCCATCGCGTGAGGG 1275
Qy 471 gcaccgagtgatgtctcgtgacgtgcacagccgctgcccgtggcggtggtgctat 530
Db 1276 GCACCGCAGTGATGGCGGTGACGTGCACAGCGCCCTGCCCGTGGCGGTGTGTCAT 1335
Qy 531 gctcatgtgagcggtggtgggtggtggtggtggtggtggtggtggtggtggtggt 590
Db 1336 GCTCATTTCTGGCGGTGGGTGGCTGCCCTGGCGGTGGGTGCTGCCCTGCCACCTCTG 1395
Qy 591 gcaactgctctgtgcttggacgctgtcagcagcagcagcagcagcagcagcagcagc 650
D 1396 GCATGCTCTGTGCGCTGGACCGCTCTCAGCGATGGCAGCCCTGCTCAGCGCTCTCTA 1455
Qy 651 ttggcgtctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 710
Db 1456 TTTGGCGGTGCGGTGCTGTCAGCGCTGTTGCTCTCTCTCTCTCTCTCTCTCTCTCT 1515
Qy 711 ccgcattttctctacgtggtggtggtggtggtggtggtggtggtggtggtggtggtg 770
Db 1516 CCGCATTTTCTTCTACGTGCGGCGGAGTGCAGCGATGGCAGAGAGATGTGAGCTGCCA 1575
Qy 771 ccccgctacagagagac 830
Db 1576 CCCCCGCTACCGAGAGACACACCTCAGCGTGTGTCAGACTGTGTGTCATCATCTCTGGGG 1635
Qy 831 gttcgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 890
Db 1636 GTTGT 1695
Qy 891 gtcctgcaatgcttctggtggtggtggtggtggtggtggtggtggtggtggtggtggt 950
Db 1696 GTCTTGCAATGCTTGGCGTTAGAAAAGTACTTCTACTGTTGGCGGAGCCCAACCTCACT 1755
Qy 951 ggtcaatgctggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1010
Db 1756 GGTCAATGCTGCTGT 1815
Qy 1011 tct-ctgtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 1069

Db 1816 TCTCTGTCTGCGGTGCTCCGCCAGTCCACCCGAGTCTGTCCACTATACATCTCTG 1875
Qy 1070 ccagggaggtgcagcactcgatcatgtctcccgagagcggccacccactgat-gact 1128
Db 1876 CCAGGGAGGTGCGCAGCAGTCCGATCATGTCTCCGAGAGAGCGCAGCCACTGTGACT 1935
Qy 1129 ccaccttagctactctgaactcagcgtgtagcgcgagcaagaataccacagccct 1188
Db 1936 CCACCTTTAGCTACCTTGAACGTACAGCGGTACGCGGCAAGCAAAATCCACAGCCCT 1995
Qy 1189 gatgactgtgggtgctcctcctggctcaacccaacc 1222
Db 1996 GATGACTTGTGGTGTCTCTCTGGCTCAACCCAACC 2029

RESULT 5

US-08-467-947A-3
Sequence 3, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPRI
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM: FLOPPY DISK
MEDIUM TYPE: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2185 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 884..2062
US-08-467-947A-3

Query Match 49.6%; Score 860.4; DB 3; Length 2185;
Best Local Similarity 97.9%; Pred. No. 2.3e-202;
Matches 914; Conservative 0; Mismatches 16; Indels 4; Gaps 4;

Qy	292	ctgctcgcaatctaggcgcgctgacct-cttcgcggcgctggcctacctctctctcat	350
Db	1097	CTCGCGCAATCTCTCGCGGCTGACCTTCCTCGCGGCGTGGCCTACCTCTTCCTCAT	1156
Qy	351	gttcacactggtcccccacagcccgaccttcacttgaggctggttctcgcgcaggg	410
Db	1157	GTTCACACT-GTCCCGGCACAGCCGACTTCACTTGAGGGCTGTCTCTGCGGAGGG	1215
Qy	411	cttgctgacacaagcctcactgctgctggcgccacactgctgggccatgcgcgtgagct	470
Db	1216	CTTGCTGGACACAACCTCACTGGTCTGCTGGCCACACTGCTGGCCATGCCGTGGAGCG	1275
Qy	471	gcaccgcagtgatgtccgtgcagctgcacagccgcctgccccgtggccgegtggtcat	530
Db	1276	GCACGCGAGTGTATGGCGCTCAGCTGCACAGCCCTGCCCGTGGCGGTGTGTAT	1335
Qy	531	gctoaatttgggcgtgtgggtggctgccccgtggcctggggctgctgcctgccacacctg	590
Db	1336	GCTAATTGGGCGTGTGGGTGGCTGCCCTGGGCTGGGGCTGCTGCCCTGCCACCTCTG	1395
Qy	591	gcactgctctgtgccctggaccgcgtgctcacgcattggcaacctgctcagcgcctcta	650
Df	396	GCATG CCTGTGTCCTGGACCGGCTCTCACGATGACACCCCTGCTCAGCGCGTCCCTA	1455
Qy	651	tttggccgtctgggctctgtgcagcctgctgtcttcttcctgctcatggtggtctgtacac	710
Db	1456	TTTGGCGCTGGGCTCTGTCCAGGCTGCTTGTCTTCCTGCTCATGGTGCTGTGTACAC	1515
Qy	711	ccgcattttcttactgctggcgcgcagctgcagcgcattggcagagcatgtcagctgccca	770
Db	1516	CCGCATTTTCTTCTACGTGCGGCGGAGTGCAGCGCATGGCAGAGCATGTACGTGCGCA	1575
Qy	771	ccccgcctacgcgagagacacgcctcagcctggtccaagactgttgtcatcatcctgggggc	830
Db	1576	CCCCCGCTACCGAGAGACACCGCTCAGCGCTGTGTCAAGACTGTGTGCATCATCCTGGGGGC	1635
Qy	831	gttcgtgtctgtgcagaccagccaggtgtactgctcctcctgattggtttaggctgtga	890
Db	1636	GTTCTGTGTCTCTGGACACCGCAGGTGTACTGTCTCTTGATGGTTTGGCTGTGTGA	1695
Qy	891	gtctgcgaatgctctggctgtagaaaagtacttctactgtgtggccgagggccaaactcact	950
Db	1696	GTCCTGCAATGTCCTGGCGTTAGAAAAGTACTTCTACTGTTGGCGCGAGCAACCTCACT	1755
Qy	951	ggccaatgctgctgtgtactcttcgcgagatgctgagatgycgcgcgcaccttcgcgcgcct	1010
Db	1756	GGTCAATGCTGTGTACTCTTGCCGAGATGCTGAGATGCGCGCGCACCTTCCGCGCGCT	1815
Qy	1011	tct-ctgctggcgtgtcctccgcagtcacccgcgcagctgttccaactataatactctctg	1069
Df	816	TCTCCTGTGTGCGCTGCTCTCCGCCAGTCCACCGCGGAGTCTGTCCACTATACATCCTCTG	1875
Qy	1070	cccaggagggtgcagcactgcatactgcttcccgcgaagcggccaccactgat-gact	1128
Db	1876	CCAGGGAGTGCCAGCACTCCGATCATGCTTCCCAGAACGGCCACCCACTGATGGACT	1935
Qy	1129	ccacccttttagctactcttgaaacttcagcgggtacgcggcgaagcaacaaatccacagccct	1188
Db	1936	CCACCTTTAGCTCTTGAACTACAGCGGTACGGCGGAAGCAACAAATCCACAGCCCT	1995
Qy	1189	gatgactgtgggtgctcctgctcaaacccaacc	1222
Db	1936	GATGACTTGGGTGCTCTGCTGCTCAACCGAAC	2029

RESULT 6

RESULT 6
US-08-763-938-1

US-08-763-938-1
: Sequence 1, Application us/08763938: Sequence I, Application
: Patent No. 6140060

Patent No. 6140060
GENERAL INFORMATION:

APPLICANT: CHUN, Jerold J. M.

APPLICANT: CHUN, Jerold J.M.
APPLICANT: HECHT, Jonathan H

```

1  TITLE OF INVENTION:  CLONED LYSOPHOSPHATIDIC ACID
2  NUMBER OF INVENTION:  RECEPTORS
3  NUMBER OF SEQUENCES:  6
4  CORRESPONDENCE ADDRESS:
5  ADDRESSSEE:  Nikaïdo, Marmelstein, Murray and Oram LLP
6  STREET:  655 15th Street, N.W., Suite 330 - G St. Lobby
7  CITY:  Washington
8  STATE:  DC
9  COUNTRY:  USA
10 ZIP:  20005-5701
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE:  Floppy disk
13 COMPUTER:  IBM PC compatible
14 OPERATING SYSTEM:  PC-DOS/MS-DOS
15 SOFTWARE:  PatentIn Release #1.0, Version #1.30
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER:  US/08/763,938
18 FILING DATE:  12-DEC-1996
19 CLASSIFICATION:  800
20 ATTORNEY/AGENT INFORMATION:
21 NAME:  JAHNS, Kristina M.
22 REGISTRATION NUMBER:  41,092
23 REFERENCE/DOCKET NUMBER:  P8074-6018
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE:  (202) 638-5000
26 TELEFAX:  (202) 638-4810
27 INFORMATION FOR SEQ ID NO:  1:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH:  2250 base pairs
30 TYPE:  nucleic acid
31 STRANDEDNESS:  single
32 TOPOLOGY:  linear
33 MOLECULE TYPE:  cDNA
34 US-08-763-938-1

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Query Match 21.0%; Score 364; DB 3; Length 2250;
Best Local Similarity 61.6%; Pred. No. 2.1e-80;
Matches 599; Conservative 0; Mismatches 370; Indels

100	Qy	cagtgctactacaacgagaccatcggtccttctctataacaacagctggcaagagctcagc	159
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160	Qy	tccactggcggcccaaggatggtgcgtggtgagctgggctgacctgaacgtgctg	219
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220	Qy	gtgctgtgaccaatctgtggttcatagcagccatcgctccaaacgcgcgttccaccag	279
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Db 774 AGTGTGGGTGGAACTGCACTGTGATATCGATCACTGTTCACACATGGCACCCCTCTAC 833
QY 640 agcgcctctattggcgtctggcgtctgtcgagcctgtctgtctctcctgctcatgtg 699
Db 834 AGTGACTCTACTAGTCTCTGGGCCATTTTCAACCTGGTGACCTTTGGTGCATGGTG 893
QY 700 gctgtgtacacccgcattttctctacgtgctggcggcagtgacgcgcagcatggcagcat 759
Db 894 GTTCTCTACGCTCACATCTTTGGCTATGTTCCGCCAGAGGACTATGAGGATGCTCCGCCAT 953
QY 760 gtcagctgccacccgcctaccagagagacacacacacacacacacacacacacacacac 819
Db 954 AGTTCGGACCCAGAGGAATCGGACACCATGATGAGCCTTCTGAAGACTGTGGTCATT 1013
QY 820 atcctggggcgtctgtctgtctgtgacacacacacacacacacacacacacacacacac 879
D' 1014 GTGCTTGGTGGCTTATTTGCTGCTGGACTCCGGGATGGTCTGTTATTGCTGGATG-- 1071
QY 880 ttaggctgtgagtcctgtgcaatgctcctggctgtgtagaagactctctactgttggccgag 939
Db 1072 -TGTGCTGCCCGAGTGGCATGCTTGGCCATGAGAGTTCCTCCCTCCTGGCCGAG 1130
QY 940 gcaactcactggtcgaatgctgctgtgctgtgctgtgctgtgctgtgctgtgctgtgct 999
Db 1131 TTCAACTCTGCTATGAACCCCATCATCTACTCTACCGCAGACAAAGAGATGAGCGCCACC 1190
QY 1000 ttccgcgcctctctgtcgtcgtgctcctcgcgcagtcacacacacacacacacacacac 1059
Db 1191 TTCAGCAGATCTGTGTTGCCAGCGCACGAGAACCTAATGGCCCCCAGGAAGCTCT 1250
QY 1060 acatcctctgcc 1071
Db 1251 GACCGCTCTGCC 1262

RESULT 7

PCT-US96-10618-1
; Sequence 1, Application PC/TUS9610618
; GENERAL INFORMATION:
; APPLICANT: Coleman, Roger
; APPLICANT: Guegler, Karl J.
; APPLICANT: Au-Young, Janice
; APPLICANT: Bandman, Olga
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOGY
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10618
; FILING DATE: 20-JUN-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,352
; FILING DATE: 20-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/567,817
; FILING DATE: 08-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Glaister, Debra J.
; REGISTRATION NUMBER: 33,888
; REFERENCE/DOCKET NUMBER: PF-0042 PCT

TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1875 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
IMMEDIATE SOURCE:
LIBRARY: Rheumatoid Synovium
CLONE: 80853
PCT-US96-10618-1

Query Match 18.7%; Score 324.4; DB 5; Length 1875;
Best Local Similarity 59.8%; Pred. No. 1e-70;
Matches 563; Conservative 0; Mismatches 376; Indels 3; Gaps 1;

QY 100 cagtgtactactaacagagaccatcgctctctctataaacacagtggaagagctcagc 159
Db 375 CAGTGTCTTACAACGAGTCCATTGCCCTCTTTTATAACCGAAGTGAAGCATCTTGCC 434
QY 160 tccactggcggcccaagagatgtgctgtgtgcaactgggctgacgcgtcagcgtgctg 219
Db 435 ACAGAAATGGAAACAGTACAGCAAGCTGCTGATGGGACATGGAATCAGCTGTTGTATCTTC 494
QY 220 gtgtgtgtgacccaatctgtgtgtcatagcaccatcgctcctcaacgcgcgtctccaccag 279
Db 495 ATCATGTGTGGCAACCTATTGGTCATGTGTGCAATCTATGTCAACCGCGCTTCCATT 554
QY 280 cccatctactactcgtcgtgcaatctgtgctgctgctgctgctgctgctgctgctgctgct 339
Db 555 CCTATTTATTACCTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 614
QY 340 ctctctctctgttccacactgttcccgcgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 399
Db 615 TTCTATCTCATGTTCAACACAGGACCCCAATACTCGGAGACTGACTGTTAGCACATGGCTC 674
QY 400 ctgcggcagggttctgtgacacacagcctcactcgtcgtggtggcgcacactgctggtccatc 459
Db 675 CTTCGTCAGGCGCTCATTTGACACAGCCTGAGCGCATCTGTGGCCAACTTACTTGCTGCTATT 734
QY 460 gccctgagctgcacccgcagtgatgtatgtcctgtcagctgcacacgcgcgcgcgcgcgcgc 519
Db 735 GCAATCGAGAGGACATTTACGGTTTTCGCGCATGCACTCCACACACAGGATGAGCAACCG 794
QY 520 cgcgtgtcatgctcattgtggcgtgtgggtggtggtggtggtggtggtggtggtggtggtg 579
Db 795 CGGTAGTGTGGTGCATTTGTGGTATCTGAGTATGAGGATGAGTATGAGTATGAGTATGAGTAT 854
QY 580 gccactcctgctcactgctcctgtgctcctgacccgtcgtcagcagcagcagcagcagcagc 639
Db 855 AGTGTGGCTGGAATCTGTGATATTGAAATTTGAAATTTGAAATTTGAAATTTGAAATTTGAA 914
QY 640 agccgtctctatttggcgcgtgtggtcgtgtgagcctgtgtgtgtgtgtgtgtgtgtgtgtgt 699
Db 915 AGTGACTCTTACTTAGTCTTCTGGGCCATTTTCAACTTTGGTGACCTTTTGTGTGTAATGGTG 974
QY 700 gctgtgtacacccgcattttctctacgtgctggcggcagtgacgcgcagcatggcagcagcat 759
Db 975 GTTCTCTATGCTCATCTTTGGGTATGTTGCCAGAGACTATGAGTATGAGTATGAGTATGAGTAT 1034
QY 760 gtcagctgccacccgcctaccagagacacacacacacacacacacacacacacacacacac 819
Db 1035 AGTTCTGGACCCCGCGGAATCGGATACCATGATGATGATGATGATGATGATGATGATGATGAT 1094
QY 820 atcctggggcgttctgt 879
Db 1095 GTGCTTGGGGCTTTATCATCTGCTGGACTCTCTGGATTTGTTTGTGTTTGTGTTTGTGTTTGT 1152


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Db 437 AAAATTTCAATTTCCCTTTTACTACCTGTGGCTAAATTTAGCTGCTGCCGATTTCTCGC 496
QY 327 gggcggtgacctctctcatgttccacactgtccccgcacagccgacgttcaact 386
Db 497 TGAATGTGCTATGTATCTGTATGTTTAAACACAGGCCCAAGTTTCAAAAACCTTTGACTGT 556
QY 387 tgagggtgttctctcgccagggcttctgggacacaaagcctcactcgtcgtggtggtccac 446
Db 557 CAACCGCTGTTCTCCGTCAGGGCTTCTGGACAGTAGTTCACCTGCTTCCCTCCACCAA 616
QY 447 actgctggccatcgccgctgagagctgcacagcagtgatgctcgtgagctgacagccg 506
Db 617 CTGTGTTGTTATGCGCTGGAGGACACATGTCAATCATCAGGATCGGGTCCATAGCAA 676
QY 507 cctgccccgtggccgctggtcatctcattgtggtggtggtggtggtggtggtggtggt 566
Db 677 CTGTGACCAAAAGAGGGTGACACTGCTCAITTTGCTTGTCTGGGCCATCGCCATTTTAT 736
QY 567 ggggtgctgctgcccactctcctggcactgctcctgctgcccctggaccgctgctcagcat 626
Db 737 GGGGGGGTCCCCACACTGGGCTGGAATGGCTTGCATGCAACATCTCTGCTGCTTCCCT 796
QY 627 ggcacccccctgctcagcgcctcctatttggccgtctctgggctctctgagcgtctgtctt 686
Db 797 GGGCCCCCATTTACAGCAGGAGTTACCTTGTGTTTCTGGACAGTGTCCAAACCTCATGGCCT 856
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Db 857 CCTCATCATGTTGTTGTTAGGGGCTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1036
QY 747 catggcagagatgctcagctgcccaccccgctaccagagagacacagcgtcagctggtcaa 806
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QY 807 gactgtgtcactcctcctggggcggttctggtggtggtggtggtggtggtggtggtggt 866
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QY 867 gctcctggtggtttaggtggtggtcctcctcaatgctcctggtggtggtggtggtggtggt 926
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QY 927 actgttggcagagcgaacactcactggtcaatgctggtggtggtggtggtggtggtggtggt 986
Db 1097 GCTGCTGGCCCTGCTCAACTCCGTCGTGAACCCCATCATCTACTCTTACAGGACGAGA 1156
QY 987 gatgcccgcacacttccgcgcctctctctgctc 1020
Db 1157 CATGTATGGCACCATGAAGAAGATGATCTGCTGC 1190
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RL P 11

US-09-997-803-3

Sequence 3, Application US/08997803

Patent No. 60571126

GENERAL INFORMATION:

APPLICANT: CHUN, Jerold J.M.

APPLICANT: GUPTA, Ashwani

APPLICANT: MUNROE, Donald G.

APPLICANT: VYAS, Tejal B.

TITLE OF INVENTION: MAMMALIAN EDG-5 RECEPTOR HOMOLOGS

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP

STREET: 655 Fifteenth Street, N.W., Suite 330

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/997,803
FILING DATE: 24-DEC-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wong, King L.
REGISTRATION NUMBER: 37,500
REFERENCE/DOCKET NUMBER: P8074-7020
TELEPHONE: (202) 638-5000
TELEFAX: (202) 638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 639 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..634
US-08-997-803-3
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Query Match 10.5%; Score 181.8; DB 3; Length 639;

Best Local Similarity 55.6%; Pred. No. 7.8e-36;

Matches 345; Conservative 0; Mismatches 275; Indels 0; Gaps 0;

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QY 356. acactgtccccgcacagccgactttcaacttgagggtgctgtcctcgcgcagggcttgc 415
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QY 416. tggacacagcctcactcgtcgtggccacactgctggccactcgcgcgtgagctgcacc 475
Db 62 TAGACACAGCGCTGACTGCTCCCTCGTCCCAATTTGCTGGTTATTGCTGTGGAAGACACA 121
QY 476. gcagtgatgctcgtgacgtgcacagccgctgccccgctggccgctggtcactgctca 535
Db 122 TGTCNATCATGAGGATGAGATGCCACAGCAACTTGTACCAAAAAGGGGTGACGCTGCTCA 181
QY 536. ttgtggcgctggtgggtggtggtggtggtggtggtggtggtggtggtggtggtggtggt 595
Db 182 TTCTGTGCTGGTGGGCCATGCCCATCTTCATGGGGGCGTCCCCACACNCTGGGATGGAATT 241
QY 596. gctcctgtgcccgtgaccgctgctcagcagcagcagcagcagcagcagcagcagcagcag 655
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Db 422 GCCCGCGGAGGGCTCCCATGAAGCTAATGAAGACAGTATGACCGCTCTTAGCGCGCTTCG 481
QY 836. tggctcgtgacacacagccagcgtggtcactcctcctcctcctcctcctcctcctcctcct 895
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QY 956. atgctgctgtgtactcttgc 975
Db 602 ACCCGCTCATCTACTGCGCG 621
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327	QY	ggggtggcctacctcttctcatgttccacactggtccccgacacagccgcgacttcaact	386
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332			
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336	DB	TGCCCACTGGTTTTCGGGGAAGGAAGTATGTTTGTGGCTCTGTCTGCCCTCAGTCTTCAG	672
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339	QY	actgctgggcatacgccgtggagctcacgcgacgtgtgatgtccgtgcagctgcacacgg	506
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342	DB	CTCTCTGTATCGGCATTTAGCGCTACATCACCATGCTGAAGATGAAGACTACACAAACGG	732
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353			
354	DB	GGGTGGCTGCCCATCATGCGGTGGAACATGCATCAGCTCGCTGTCCAGCTGCTCCACCGT	852
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357	QY	ggcacccctgtcaagccgctcctatttggccgtctgggctgtgtgagccgtgtgtgtctt	686
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359			
360	DB	GTCCCGCTCTACCAACAAGCACTATATTCTCTGTGCAACCAACCGCTTTCACCGTGCCT	912
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363	QY	cctgctcatggttggctgtgtacaccgcgatttcttctacgtgcggcggcgagtgcagcg	746
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365	DB	GCCTTCCATCGTCCATCTCTACTGTCAGGATCTACTCTCTTGGTAGGACTCGAAGCGCCG	972
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368	QY	catggc-----agagcatgtcagctgtcaccccccgctacagagagacagcgtcagcct	800
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371	DB	CTTGACCTTCCGCAAGAATCTCCAAAGCCAGCGCGAGTTCCGAGAAAGTCTCTGGCGCTT	1032
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374	QY	ggtcaagactggtgtcatcactcctggggcgttgggtgtgtctgtctgtgacacacagggcagg	860
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377	DB	GCTGAACAGATGATTTGCTCTGAGTGTCTTCAATTGCCGTGCGGGCCCTCTCTTCAT	1092
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380	QY	ggtactgctcctggatgggttttaggtgtgtg---agtcctgcaatctcctggctgtgaaaa	917
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383	DB	CTTACTACTTTTAGATGTGGGTGCAAGCGAAGACCTGTGACATCTCTGTACAAAGCAGA	1152
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386	QY	gtacttctcactgttggccgagcccaactcactggtcaatgctgctgtgtactcttgcg	977
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388			
389	DB	GTACTTCTTGGTCTTGGCTGTGCTGAATCTAGTACCAAGCCCAATCATCTACACTGTGAC	1212
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391			
392	QY	agatgctgagatgcgcgcaccttccgcgccttctctgtgt	1019
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394	DB	CAATAAGAGAGATCGCGCGGCTTTCATCAGATCATATCTTGT	1254

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US-08-760-936-3
ence 3, Application US/08760936
ent NO. 5856443
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08760936
FILING DATE: December 6, 1996

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CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-1000C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2232 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 269..1420
J5-08-760-936-3

Query Match	9.4%	Score 163.2	DB 2	Length 2232	
Best Local Similarity	51.7%	Prod. NO. 4.4e-31			
Matches 425	Conservative	0	Mismatches 388	Indels 9	Gaps 2
Qy	207	cgtcagcgtgctggtcgtgaccaaactcgtcgtgctatagcagccatcgctccaacg	266		
Db	433	CATCGCTGCTGATCATCCTAGAGAAATATTGCTCTGTCTTAATATTGGAAACCAA	492		
Qy	267	ccgcttcaccagcccatctactactcgtcgtcggaactggtccggtgacctcttcgc	326		
Db	493	GAAGTTCACCGGCCCATGTACTATTTCATAGGCAACCTAGCCCTCTGGACCTGTAGC	552		
Qy	327	gggggtgcctacactctctctctatgttccacactggtcccccagacgccgcagcttcaat	386		
Db	553	AGGATGCTGTACACAGCTAACTCTGTGTCTGGGCCACCACTTACAAGCTCACACC	612		
Qy	387	tgaggctggcttcctgcgcagcaggctcgtggacaaagcactcaactggtcgtggccac	446		
Db	613	TGCCCAGTGGTTCGCGGGGAAGGATGTGTTGTGGCTCTGTCTGCCCTCAGCTTTCAG	672		
Qy	447	actgctggccatcgccgtggagctgcacgcagtgatgtccgtgcagctgcacagcgg	506		
Db	673	CCTCCTTGTATCGCATTTGAGCGCTACATCACCATGCTGAAGATGAACATACACAACGG	732		
Qy	507	cctgcgcccgctggcccgctggctatgctcattgtgggcgtgtgggtggtgcctggggct	566		
Db	733	CAGCAACAGCTGGCGCTCCTTCTCTGCTGATCAGTGCCTGCTGGGTCATCTCCCTCATCCT	792		
Qy	567	ggggctgctgctgcgcactcctgcactgctctgtgccttgaccgtgctcagcat	626		
Db	793	GGTGGGCTGCCCATCATGGGTGGAACCTGCATCATGCTGCCTGCTCCACCTT	852		
Qy	627	ggcaccctgctcagccgctcctattggccgctcgtgggcctgtgcagcctgctctgttt	686		
Db	853	GCTCCCGCTCTACCAACAAGCACTATATCTCTCTGCACCAACCGCTCTTCAACCTGCTCT	912		
Qy	687	cctgctcatggtggctggtacacccgcattttcttctacgtgctggcgccagtgacgg	746		
Db	913	GCTTTCCATCGCTATCCCTCTACTGAGGATCTACTCTTGGTGGAGGACTCGAAGCGCCG	972		
Qy	747	catggc-----agagcatgctcagctgccaaccccgctaccgagagaccagctcagcct	800		
Db	973	CCTGACCTTCGCAAGAACATCTCAAGGCCAGCGCAGTTCGAGAAAGCTCTGTGGCCCTT	1032		
Qy	801	ggccaagactgtgtcatcatcctggggcgcttcgtgtcgtctgtgacaccagggccaggt	860		
Db	1033	GCTGAAGACAGTGATCATTTGCTCAGTGTCTTCATTGCTCTGSGGCCCTCTCTTCAT	1092		
Qy	861	ggtaactgctcgtggatggttttagcgtgtg---agtcctgcaatgtcctggctgtgaaaa	917		
Db	1093	CCTACTACTTTTAGATGTGGGTGGCAAGCGAAGACCTGTGATCATCTGTACAAAGCAGA	1152		

Db	61	NSXFHSNYFLG	NLAASDLLAGVAVANTLLSGPVTLSLTPLOWFARBCGSAFITUSAY	120
QY	121	GSLLATAIERHVA	IAKYKLYGSKSCRMILLIGASMLISLVIGGLPTILGWNCGLHDEACS	180
Db	121	FSLLAATAIERQVA	IAKYKLYGSKSCRMILLIGASMLISLVIGGLPTILGWNCGLHDEACS	180
QY	181	TVLPLYAKHYVLC	WVTIFSIILLIAIYALYVRIYCVVRSRHADMAAPOTLALLKTVTVIVLG	240
Db	181	TVLPLYAKHYVLC	WVTIFSVILLIAIYALYVRIYFVVRSSHADYAGPOTLALLKTVTVIVLG	240
QY	241	VFIICWLPAPFS	ILLDDYACPVHSCPTILYKAHYFFAVSTLNSLNLNPVIYTWRSRDLARREV	300
Db	241	VFIICWLPAPFS	ILLDDSTCPVRACPVLYKAHYFFAATLNSLNLNPVIYTWRSRDLARREV	300
QY	301	RPLOCWRP	GVGVGRRRGVTPGHHLIPLRSSSSLERGMHMTSPTFLEGNVTV	353
Db	301	RPILLCWROG	KAGYGRGRC-GNPGHRLIPLRSSSSLERGLHMTSPTFLEGNVTV	352

References

```

: Sequence 4, Application US/08196989B
: Patent No. 5583476
: GENERAL INFORMATION:
: APPLICANT: MacLennan, A. John
: TITLE OF INVENTION: Molecular Cloning and Expression of
: TITLE OF INVENTION: G-Protein Coupled Receptors
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Saliwanchik & Saliwanchik
: STREET: 2421 N.W. 41st Street, Suite A-1
: CITY: Gainesville
: STATE: FL
: COUNTRY: US
: ZIP: 32606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/196,989B
: FILING DATE: 15-FEB-1994
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Lloyd, Jeff
: REGISTRATION NUMBER: 35,589
: REFERENCE/DOCKET NUMBER: MAC-100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 904-375-8100
: TELEFAX: 904-372-5800
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 383 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: US-08-196-989B-4

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Query Match          46.1%; Score 834; DB 1; Length 383;
.Best Local Similarity 48.4%; Pred. No. 2.1e-62;
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[illegible]

[illegible]

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RECUIT 4
U -760-936-4
, uence 4, Application US/08760936
Patent No. 5856443
GENERAL INFORMATION:
APPLICANT: MacLennan, A. John
TITLE OF INVENTION: Molecular Cloning and Expression of
TITLE OF INVENTION: G-Protein Coupled Receptors
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: US
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08760,936
FILING DATE: December 6, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Doran R.
REGISTRATION NUMBER: 38,261
REFERENCE/DOCKET NUMBER: MAC-100C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 383 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-08-760-936-4

```

[illegible]

```

QY 182 VLPLYAKHYVLVVTFISIIALLAIVALYVRIYCVBS-----SHADMAAPQTLA 230
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 195 VLPLYKHYILFCTTFTVLGLLSIVLYCRIYSLVTRSRRLTFRKNISKRSEKSLA 254
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 231 LLKTVTIVLGVFVCMPLAFSIIILDDYACPVHSCPILYKAHFVFFAVTSLNLNPVIYTW 290
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 255 LLKTVIIVLSVFACIAPLEFILLLLLDVGCKAKTCDILYKAELFVLVAVLNSGTNPIIYTL 314
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 291 RSRDLREVLRLPQCNWR-PGVGVQGR-RRVGTGPHHLLPLRSSSS 333
      :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
Db 315 TNKEMRAFRIRIISCKCPNGDSAGFKRPIIPGMEFSRKSQDNS 359
      :|||: |||: |||: |||: |||: |||: |||: |||: |||: |||:

RESULT 5
US-08-845-566-3
; Sequence 3, Application US/08845566
; Patent No. 5912144
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl
; TITLE OF INVENTION: EDG-1 LIKE RECEPTOR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/845,566
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:

```

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0271 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 181948
US-08-845-566-3

	Query Match	45.5%;	Score 823.5;	DB 2;	Length 381;	
	Best Local Similarity	49.7%;	Pred. No. 1.5e-61;			
:	Matches 156;	Conservative 59;	Mismatches 88;	Indels 11;	Gaps 2;	
QY	3	SLYSEYLNPKNKVOEHNYNT-KETLETOETTSSROVASAGIVILCCAAIVVENLLVIAVARN	61			
		: : : :	: : : :	: : : :	: : : :	
Dd	14	SSYSVDVNYDIIVRHNYNTGKLMSADKENSIKLTSVVFIILCCFIIILETFVLLTIWKT	73			
		: : : :	: : : :	: : : :	: : : :	
QY	62	SKEFSAMYFLGNLAASDLLAGVAFAVANTLLSGSVTLRLTPVQMFAREGSATISLSAVG	121			
		: : : :	: : : :	: : : :	: : : :	
Dd	74	KKEHREPMYFYIGNLALSDLLAGVAYTANLLSGATTYKLTPAQWFLEGSMFEVALSASF	133			
		: : : :	: : : :	: : : :	: : : :	
QY	122	SLLAIAIERHVAATAKYLCSCSKRCMILLIGASWLISLVUGGPPIGLWGNCGLHLEACST	181			
		: : : :	: : : :	: : : :	: : : :	

Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, CRAMER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
~467-947A-28

Query Match 45.5%; Score 823.5; DB 3; Length 381;
Best Local Similarity 49.7%; Pred. No. 1.5e-61;
Matches 156; Conservative 59; Mismatches 88; Indels 11; Gaps 2;
QY 3 SLYSEYLNPNKVOEHYNYT-KETLETOETTSRQVASAGIVILCCAIYVENLLVLIYARN 61
Db 14 SSVSDYVNYDIIVRHNYTGKLNISADKENSIKLTSVVFILICCFILENIFVLLTIWKT 73
QY 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSASITLSASVG 121
Db 74 KKFHRPMYFIIGNLADSLLAGVAYTANLLSGATTYKLTTPAQWFLREGSMFVALSASF 133
QY 122 SLAIAIERHVAIAKVKLYGCKSCRMILLIGASWLSILVLGGLPILGWNCGLHLEACST 181
Db 134 SLAIAIERYITMLKMKLHNGSNFRLLISACWVLSILGGLPIMGWNCISALS SCSCT 193
QY 182 VLPLYAKHYVLCVVTTFISIIAIAVLYRIYCVWRSSHADMA-----APOTLAL 231
Db 194 VLPLYKHKVILFCTVTFITLISIVILYCRISLVRTSRRLTFKRNISKASRSSENVAL 253
QY 232 LKTIVTLGVFVVCWLPAPFASILLDDYACPVHSPILYKAYHFAVSTLNSLLNPVIYTW 291
Db 254 LKTIVTLVSVFIACWAPFLFILLDDVGCKVKTKDILFRAEYFLVLAVALNSGTNPVIYTLT 313
QY 292 SRDLREVLRLPQC 305

Db 314 NKEMRRAPIRIMSC 327
RESULT 9
PCT-US96-10618-4
Sequence 4, Application PC/TUS9610618
GENERAL INFORMATION:
APPLICANT: Coleman, Roger
APPLICANT: Guegler, Karl J.
APPLICANT: Au-Young, Janice
APPLICANT: Bandman, Olga
APPLICANT: Seilhamer, Jeffrey J.
TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10618
FILING DATE: 20-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/000,352
FILING DATE: 20-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/567,817
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Glaister, Debra J.
REGISTRATION NUMBER: 33,888
REFERENCE/DOCKET NUMBER: PF-0042 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 381 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 119130
PCT-US96-10618-4

Query Match 45.5%; Score 823.5; DB 5; Length 381;
Best Local Similarity 49.7%; Pred. No. 1.5e-61;
Matches 156; Conservative 59; Mismatches 88; Indels 11; Gaps 2;
QY 3 SLYSEYLNPNKVOEHYNYT-KETLETOETTSRQVASAGIVILCCAIYVENLLVLIYARN 61
Db 14 SSVSDYVNYDIIVRHNYTGKLNISADKENSIKLTSVVFILICCFILENIFVLLTIWKT 73
QY 62 SKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQVFAREGSASITLSASVG 121
Db 74 KKFHRPMYFIIGNLADSLLAGVAYTANLLSGATTYKLTTPAQWFLREGSMFVALSASF 133
QY 122 SLAIAIERHVAIAKVKLYGCKSCRMILLIGASWLSILVLGGLPILGWNCGLHLEACST 181
Db 134 SLAIAIERYITMLKMKLHNGSNFRLLISACWVLSILGGLPIMGWNCISALS SCSCT 193

[illegible]

RESULT 12
 PCT-US93-08528-73
 Sequence 73, Application PC/TUS9308528
 GENERAL INFORMATION:
 APPLICANT: New York University
 TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
 TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
 NUMBER OF SEQUENCES: 348
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BROWDY AND NEIMARK
 STREET: 419 Seventh Street, N.W., Suite 300
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20004
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/08528
 FILING DATE: 09-SEP-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/943,236
 FILING DATE: 10-SEP-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Townsend, Kevin G.
 REGISTRATION NUMBER: 34,033
 REFERENCE/DOCKET NUMBER: MURPHY-2 PCT
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-628-5197
 TELEFAX: 202-737-3528
 TELEX: 248633
 INFORMATION FOR SEQ ID NO: 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 334 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 PCT-US93-08528-73

Query Match 41.4%; Score 749; DB 5; Length 334;
Best Local Similarity 48.6%; Pred. No. 2.3e-55;
Matches 142; Conservative 57; Mismatches 81; Indels

[illegible]

Query Match 29.1%; Score 526; DB 5; Length 393;
Best Local Similarity 35.7%; Pred. No. 1.3e-36;
Matches 121; Conservation 70.0%;

	Matches	121;	Conservative	70;	Mismatches	116;	Indels	32;	Gaps	10;
Qy	18	YNYTKETLEQ-	E-TTSRQVASGIVILCCAI	VVENLVLVIAVRNSKFHSAMYLFLGNLA	76					
		:	:	:	:	:	:	:	:	:
Db	34	YNRSKGLATEWNTSVKLVMGLGITV-CIFIMLANLLVMVAIYVNRHFSPYYLMANLA	92							
		: :	:	:	:	:	:	:	:	:
Qy	77	ASDLLAGVAFVANTLLSGSVTLRLTPVQWFARGSSITLSASVGSLLAIAIERHVAIAK	136							
		: : :	:	:	:	:	:	:	:	:

Db 93 AADFFAGLAYFYLMFNTGPNTRRLTVSTWLLRQGLDITVTASVANLLAIAIERHITVFR 152

Qy 137 VKLYGSKSCRMILLIGASWLSISVLGGLPILGWNCLHLEACSTVPLVYAKHYVLCVVT 196

Db 153 MOLHTRMSNRVVVVVITWMAIVMGAIPTSVGWNCICIDHCNSNMAPLYSDSY-LVFWA 211

Qy 197 IFSII-LIAIYALVYRIYCVVR-----SSHADMAPO-----TLALLKTVIIVLGAFIV 244

Db 212 IFNLVTFVVMVYLAHIFGYVRQRTMRMSRHS--SGPRNRDRTMMSLLKTVIIVLGAFIV 269

Qy 245 CWLPAFSLILLDYACPVHSCPIYKAHYFFAVSTLNSLLNPVIYTWRSRLRREVLRPQ 304

Db 270 CWTGCLVLLLDVCCP--QCDVLAYPEKFFLLAEFNSAMNPIIYSYRDKEMSATFRQILC 327

Qy 305 CWRPGVGVQRRRVGTPGHLLPLRSSSSLER----GMH 339

Db 328 C-----QRSENTSGPTGSDRSASSLNHTILAGVH 357

RESULT 14

US-08-763-938-2

Sequence 2, Application US/08763938

Ent No. 6140060

GENERAL INFORMATION:

APPLICANT: CHUN, Jerold J.M.

APPLICANT: HECHT, Jonathan H.

TITLE OF INVENTION: CLONED LYSOPHOSPHATIDIC ACID

TITLE OF INVENTION: RECEPTORS

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Nikaido, Marmelstein, Murray and Oram LLP

STREET: 655 15th Street, N.W., Suite 330 - G St. Lobby

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/763,938

FILING DATE: 12-DEC-1996

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: JAHNS, Kristina M.

REGISTRATION NUMBER: 41,092

REFERENCE/DOCKET NUMBER: P8074-6018

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 638-5000

TELEFAX: (202) 638-4810

FORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 364 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-763-938-2

Query Match 28.9%; Score 523; DB 4; Length 364;

Best Local Similarity 35.7%; Pred. No. 2.le-36;

Matches 116; Conservative 71; Mismatches 116; Indels 22; Gaps 9;

Qy 18 YNYTKETLETO-ETTSQVASAGIVILCCAVENLLVLAIVARNKFSAMVLFGLNLA 76

Db 34 YNRSGLATEMTWVSKLVMLGITV-CVFIMLANLLVMVAIVYVRRFHPFIYVLMANLA 92

Qy 77 ASPLLGAFAVANTLLSGSVTLRLTPVQWFARECSATITLSASVGSLLATAIERHVAIAK 136

Db 93 AADFFAGLAYFYLMFNTGPNTRRLTVSTWLLRQGLDITVTASVANLLAIAIERHITVFR 152

Qy 137 VKLYGSKSCRMILLIGASWLSISVLGGLPILGWNCLHLEACSTVPLVYAKHYVLCVVT 196

Db 153 MOLHTRMSNRVVVVVITWMAIVMGAIPTSVGWNCICIDHCNSNMAPLYSDSY-LVFWA 211

Qy 197 IFSII-LIAIYALVYRIYCVVR-----SSHADMAPO-----TLALLKTVIIVLGAFIV 244

Db 212 IFNLVTFVVMVYLAHIFGYVRQRTMRMSRHS--SGPRNRDRTMMSLLKTVIIVLGAFIV 269

Qy 245 CWLPAFSLILLDYACPVHSCPIYKAHYFFAVSTLNSLLNPVIYTWRSRLRREVLRPQ 304

Db 270 CWTGCLVLLLDVCCP--QCDVLAYPEKFFLLAEFNSAMNPIIYSYRDKEMSATFRQILC 327

Qy 305 CWRPGVGVQRRRVGTPGHLL 326

Db 328 CORNENPNGPTGSDRSASSLNHTI 352

RESULT 15

PCT-US96-10618-2

Sequence 2, Application PC/TUS9610618

GENERAL INFORMATION:

APPLICANT: Coleman, Roger

APPLICANT: Guegler, Karl J.

APPLICANT: Au-Young, Janice

APPLICANT: Bandman, Olga

APPLICANT: Seilhamer, Jeffrey J.

TITLE OF INVENTION: A NOVEL HUMAN EDG-2 RECEPTOR HOMOLOG

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10618

FILING DATE: 20-JUN-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/000,352

FILING DATE: 20-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/567,817

FILING DATE: 06-DEC-1995

ATTORNEY/AGENT INFORMATION:

NAME: Glaister, Dendra J.

REGISTRATION NUMBER: 33,888

REFERENCE/DOCKET NUMBER: PF-0042 PCT

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-855-0555

TELEFAX: 415-845-4166

TELEX:

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 364 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: Rheumatoid Synovium

CLONE: 80853

PCT-US96-10618-2

Query Match 28.9%; Score 523; DB 5; Length 364;

Best Local Similarity 35.7%; Pred. No. 2.le-36;
Matches 116; Conservative 71; Mismatches 116; Indels 22; Gaps 9;

QY	18	YNYTKETLEQ-ETTSRQVASAGIVILCCAIWENLLVLIAVARNKPFHSAMYLFLGNLA	76
Db	34	YNRSGKHLATEWNTVSKLVWCLGTV-CIFIMLANLLVMVAIYVNRFRFFIYYLMA	92
QY	77	ASDLLACVAFVANTLLSGSVTLRLTPQWFAREGSASTLSASVGSLLAIAIERHVAIAK	136
Db	93	AADFFAGLAYFYLMFNTGPNTRLTVSTWLLRQGLIDTSLTASVANLLAIAIERHITVFR	152
QY	137	VKLYGCKSCRMULLIGASWLISLVGLPLTILGNCLHLEACSTVPLPIYAKHYVLCVVT	196
Db	153	MLHTRMSNRVVVIVVITMAIVMGAIPSVGNWCIDICNSMAPLYSDSY-LVFWA	211
QY	197	IFSII-LLAIVALYVRIYCVVR-----SSHADMAAPQ-----TLALKVTIVILGVFIV	244
D'	212	IFNLVTFVVMVLYAHIFGVVQRTMRMSRHS---SGPRRNPDTMMSLLKTVVIVLGGFII	269
QY	245	CWLPAPFILLDDYACPVHSCPILYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVLRLPQ	304
Db	270	CWTPGLVLLLDVCCP--QCDVLAYEKFFLLAEFNSAMNPITYSYRDKEMSATFRQILC	327
QY	305	CWR---PGVGVQGRRRVGTGCHLL	326
Db	328	QRSENPTAPTEGSDRSASSLNHTI	352

Search completed: December 20, 2001, 10:46:09
Job time: 2218 sec

1;

Qy	902	tcttggtgtgagaaagtacttccctactgtgtgcccagggcgaactcactggtcaatgctg	961
Db	994	TCTTGGCTGTAGAAAAGTACTTCTTACTGTGTGCCGAGGCCAACTCACTGGTCAATGCTG	1053
Qy	962	ctgtgtactcttggcagatgctgagatgctgcgcgcaccltccggcgccttctctgtgctgcg	1021
Db	1054	CTGTGTACTTTCGCGAGATGCTGAGATGCGCGCACTTCCGCCGCTTCTCTGTCTGCTGC	1113
Qy	1022	ctgtgctccgccagtcacccgcgcgagctgttcacatatacatcctctgcgccaggaagtg	1081
Db	1114	CGTGCTCCGCCAGCCACCCGCGAGTCTGTCCACTATACATCTCTGCCCAGGGAGGTG	1173
Qy	1082	ccagcactgcatactgtctcccgagaaaggccacccactgat-gactccacccctttagc	1140
Db	1174	CCAGCACTCGCATCATGCTTCCGAGAGCGGCACCCACTGATGGACTCCACCCTTTAGC	1233
Qy	1141	taccttgaacttcagcggtagcggcgaagcaacaataccacagccctgatgacttgttg	1200
Db	1234	TACCTTGAACCTTACCGGTACGGCGCAAGCAACAATCCACAGCCCTCATGACTTTGTGG	1293
Qy	1201	gtgtctctggctcaacccaaaccaagactgactgactggcaggacaaggtcttgcatg	1260
Db	1294	GTGTCTCTGGCTCAACCCACCAACAGGACTGACTACCGCGCAGGACAAGGTCTGCATG	1353
Qy	1261	gcacagcacactaccagggctcccccaggcacacacactctgccagggaatgggggcttt	1320
Db	1354	GCACAGACCACTGCCAGGCTTCCCCAGGCACACCACTGTGCCAGGGAATGGGGGCTTT	1413
Qy	1321	gggtcatctccactgcctgggggagtcagatggggtcagaaactcgtctcttcagcca	1380
Db	1414	GGGTCACTCCCACTGCTTGGGGGACTCAGATGGGGTCAGGAATCGCTCTTCAGCCA	1473
Qy	1381	tctcaggtttagggggtttgtaacagacattattctgttttcactgcgtatcctttggtaa	1440
Db	1474	TCCCAGGTTTAGGGGGTTTGTAAACAGACATTATTCTGTCTTTCACATGCGTATCCTTGGTAA	1533
Qy	1441	gccctggagactggttaatgctgtgtgactgaggggttttaaggtggggagagataag	1500
Db	1534	GCCCTGTGGACTGTCTCTGTGTGTATGCTGAGGGTTTTTAAGGTGGGAGAGATAAG	1593
Qy	1501	gctctctgggccaatgctaccccggtatgactgggttaatgagacagactgtggacaaccc	1560
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Qy	1681	tcacggggggggatgatatacaaggagttaaacctttctttacatc	1726
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RESULT 2

US-08-760-936-2

Sequence 2, Application US/08760936

Patent No. 5856443

GENERAL INFORMATION:

APPLICANT: MacLennan, A. John

TITLE OF INVENTION: Molecular Cloning and Expression of

TITLE OF INVENTION: G-Protein Coupled Receptors

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: US

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/760.936

FILING DATE: December 6, 1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Pace, Doran R.

REGISTRATION NUMBER: 38,261

REFERENCE/DOCKET NUMBER: MAC-100C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 352-375-8100

TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 352 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-760-936-2

Query Match 87.8%; Score 1589.5; DB 2; Length 352;
Best Local Similarity 88.7%; Pred. No. 1.1e-125;
Matches 313; Conservative 13; Mismatches 26; Indels 1; Gaps 1;

Qy 1 MGSLEYSEYLNPNKQVEHYNYTKETLETQETTSRQVASAGIVILCCAIVVENLLVLIAR 60
Db 1 MGSLEYSEYLNPNKQVEHYNYTKETLDMQETPSRKVASAFIILCCAIVVENLLVLIAR 60
Qy 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGSVTLRLTPVQWFAREGSASITLSASV 120

wed n.

Db 61 NSKFHSAMYLFLGNLAASDLLAGVAFVANTLLSGPVTLSLTPLQWFAREGSASITLSASV 120
Qy 121 GSLLAIAIERHVAIAKVKLYGSKSCRMLLLIGASWLISLVLGGPILGWNCLEHLEACS 180
Db 121 FSLLAIAIERQVAIAKVKLYGSKSCRMLLLIGASWLISLVLGGPILGWNCLEHLEACS 180
Qy 181 TVLPLYAKHYVLCVVTIFSIILLAIVALYVRIYCVVRSSHADMAAPQTLALLKTVTIVLG 240
Db 181 TVLPLYAKHYVLCVVTIFSVILLAIVALYVRIYFVVRSSHADVAGPQTLALLKTVTIVIG 240
Qy 241 VFIVCWLPAPFSILLDDYACPVHSCPIYKAHYFFAVSTLNSLLNPVIYTWRSRDLRREVL 300
Db 241 VFIICWLPAPFSILLDDSTCPVRACPVLYKAHYFFAFATLNSLLNPVIYTWRSRDLRREVL 300
Qy 301 RPLQCWRPGVGQVQRRRVGTPGHLLPLRSSSSSLERGMHMTSPTFLEGNTVV 353
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RESULT 3

US-08-196-989B-4

1400

Wed

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Best Local Similarity 82.2%; Pred. No. 1.4e-146;
Matches 811; Conservative 0; Mismatches 173; Indels 3; Gaps 1;

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Qy	196	gccatttggtgtggaacacctcttggtgtctcattgcggtggccggaacagcaagttccac	255
Db	283	GCCATCGTGGTGGAGAACCTTCTGGTGCTAATCGCAGTGGCCAGGAACAGCAAGTCCAC	342
Qy	256	tcggcaatgtacctgtttctgggcaacctggccgcctccgatctactggcaggcggtggcc	315
Db	343	TCAGCCATGTACTGTTCCTCGGCAACCTGGCAGCCTCCGACCTGCTGGCAGGCGTGGCC	402
Qy	316	ttcgtagccaataddttgctctctgtgctctgtcacgctgaggtgtgacgcctgtgcagtgg	375
Db	403	TTCGTGGCCAACACCTTGCTCTCCGACCTGTCAACCTGTCTTAACCTCCCTGCAGTGG	462
Qy	376	tttgccgggagggtctctgctccatcacgctctcgccctctgtcttcagcctcctggcc	435
Db	463	TTTGCCCGAGAGGGTTTCAGCCTTCATCACGCTCTCTGCTCGGTCTTCAGCCTCTCGCC	522
Qy	436	atcgccattgagcgccacgtggccattgccaagggtcaagctgtatggcagcgacaagagc	495
Db	523	ATTGCCATCGAGAGACAAGTGGCCATCGCCAAGGTCAAGCTCTACGGCAGTGACAAAAGC	582
Qy	496	tgccgcgatgcttctgtctcatcgggggcctcggtggtcatctcgctggtctcctgggtggtc	555
Db	583	TGTCGAATGTTGATGCTCATTTGGGGCCTCTTGCTGATATCGCTGATTTCTGGGTGGCTTG	642
Qy	556	cccatccttggtgtggaactgcctggggccacctcgaggcctgtgccactgtcctgcctctc	615
Db	643	CCCATCTTGGGCTGGAATTGTCTGGACCATCTGGAGGCTTGCTCCACTGTGCTGCCCTC	702
Qy	616	tacgccaagcattatgtgtgtgtgctgtgacctcttctccatcatcctgttggccatc	675
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Wed Dec 26 09:32:47 2001

us-09-274

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Db 763 GTGGCCTTGTAAGTCCGAATCTACTTCGTAGTCCGCTCAAGCCATGCGGACGTTGCTGGT 822
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Qy 736 ccgcagacgctagccctgctcaagacgggcaccatcgctagggcgtctttatcgctgc 795
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Db 823 CCTCAGACGCTGGCCCTGCTCAAGACAGTCACCATCGTACTGGGTGTTTCATCATCTGC 882
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Qy 796 tggctgcccgccttcagcatcctcctcttggaactatgcctgtcccgccactcctgcccg 855
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Qy 856 atcctctacaaagcccactactttttcgccgtctccaccctgaattcctgctcaacccc 915
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Qy 916 gtcactctacacgtggcgagccgggacctgcggcgagggtgcttcggccgctgcagtgc 975
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Qy 1036 ctgccactccgcagctccagctccctggagaggggcatgcacatgcccacgtcaccacg 1095
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Qy 1096 tttctggagggaacacacggtggtctga 1122
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Db 1180 TTTCTGGAGGGCAACACAGTGGTCTGA 1206
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RESULT 3
US-09-00000000
Seque

ALIGNMENTS

RESULT : 1
 US-08-861-747-1
 ; Sequence 1, Application US/08861747
 ; Patent No. 6020158
 ; GENERAL INFORMATION:
 ; APPLICANT: MUNROE, Donald G.
 ; APPLICANT: VYAS, Tejal B.
 ; TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
 ; NUMBER OF SEQUENCES: 7
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
 ; STREET: 655 15th St., NW, Suite 330 - G Street Lobby
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005-5701
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/861,747
 ; FILING DATE: 22-MAY-1997
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jahns, Kristina M.
 ; REGISTRATION NUMBER: 41,092
 ; REFERENCE/DOCKET NUMBER: P8074-7003
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 638-5000
 ; TELEFAX: (202) 638-4810
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1761 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: double
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 US-08-861-747-1

Query Match 96.9%; Score 1680; DB 3; Length 1761;
 Best Local Similarity 98.7%; Pred. No. 0;
 Matches 1703; Conservative 1; Mismatches 21; Indels 1; Gaps 1;

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RESULT 2

US-08-861-747-3
: Sequence 3, Application US/08861747
: Patent No. 6020158
: GENERAL INFORMATION:
: APPLICANT: MUNROE, Donald G.
: TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
: STREET: 655 15th St., NW, Suite 330 - G Street Lobby
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-5701
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/861,747
: FILING DATE: 22-MAY-1997
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Johns, Kristina M.
: REGISTRATION NUMBER: 41, 092
: REFERENCE/DOCKET NUMBER: P8074-7003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 638-5000
: TELEFAX: (202) 638-4810
: INFORMATION FOR SEQ ID NO: 3:

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/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-870-511-5 + 286.50 562.93 1.0e-23 1671
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-861-747-1

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seq_documentation_block:
; Sequence 1, Application US/08861747
; Patent No. 6020158
; GENERAL INFORMATION:
; APPLICANT: MUNROE, Donald G.
; APPLICANT: VYAS, Tejal B.
; TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
; STREET: 655 15th St., NW, Suite 330 - G Street Lobby
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/861,747
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jahns, Kristina M.
; REGISTRATION NUMBER: 41,092
; REFERENCE/DOCKET NUMBER: P8074-7003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1761 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-861-747-1
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Quality: 1941.00 Length: 383
Ratio: 5.094 Gaps: 1
Percent Similarity: 99.478 Percent Identity: 98.956
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141 TAACAACAGTGGCAAAGAGCTCAGCTCCCACTGGCGGCCCAAGGATGTGG 190
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441 GTGGGTGGCCACACTGCTGCCATCCCGTGGACGACCGACGAGTGA 490
134 etAlaValGlnLeuHisSerArgLeuProArgGlyArgValValMetLeu 150
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151 ileValGlyValTrpValAlaAlaLeuGlyLeuGlyLeuLeuProAlaHi 167
541 ATTGGGGCTGGTGGTGGCTGCCCTGGCGCTGGCGCTGTTGCCTGCCCA 590
167 sSerTrpHisCysLeuCysAlaLeuAspArgCysSerArgMetAlaProL 184
591 CTCTGGCACTGCTGCTGGCTGGCTGGCGCTGCTCAGCATGGCACCCC 640
184 euLeuSerArgSerTrpLeuAlaValAlaTrpAlaLeuSerSerLeuVal 200
641 TGCTCAGCGCTCCTATTGGCGCTGCTGGCTGCTGCAGCGCTGTTGTC 690
201 PheLeuLeuMetValAlaValTrpThrArgIlePhePheTrpValArgAr 217
691 TTCTGCTCATGGTGGCTGTGACACCGCATTTTTTATACGTGCGGCG 740
217 qArgValGlnArgMetAlaGluHisValSerCysHisProArgTrpArgG 234
741 GCGAGTGCAGCCATGGCAGACATGTGAGTGCACCCCGCTACCGAG 790
234 luThrThrLeuSerLeuVallyThrValValIleLeuGlyAlaPhe 250
791 ACACCAAGCTCAGCTGCTGCAAGACTGTTGTCATCATCTCTGGGCGCTC 840
251 ValValCysTrpThrProGlyGlnValValLeuLeuLeuAspGlyLeuGl 267
841 GTGGTCTGCTGGACACCGCGGCTGCTGCTGCTGCTGCTGCTGCTGCT 890
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: Sequence 3, Application US/08861747
: Patent No. 6020158
: GENERAL INFORMATION:
: APPLICANT: MUNROE, Donald G.
: APPLICANT: VYAS, Tejal B.
: TITLE OF INVENTION: A HUMAN EDG-6 RECEPTOR HOMOLOG
: NUMBER OF SEQUENCES: 7
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nikaido, Marmelstein, Murray & Oram LLP
: STREET: 655 15th St., NW, Suite 330 - G Street Lobby
: CITY: Washington
: STATE: DC
: COUNTRY: USA
: ZIP: 20005-5701
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/861,747
: FILING DATE: 22-MAY-1997
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Jahns, Kristina M.
: REGISTRATION NUMBER: 41,092
: REFERENCE/DOCKET NUMBER: P8074-7003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 638-5000
: TELEFAX: (202) 638-4810
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1889 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
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DEFINITION Homo sapiens G protein-coupled receptor Eag-4 mRNA, complete cds.
ACCESSION AF011466
VERSION AF011466.1 GI:2735848
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM

REFERENCE 1 (bases 1 to 1734)
AUTHORS An.S., Bleu.T., Hallmark.O.G. and Goetzl.E.J.
TITLE Characterization of a novel subtype of human G protein-coupled receptor for lysophosphatidic acid
J. Biol. Chem. 273 (14), 7906-7910 (1998)
MEDLINE 98192573
REFERENCE 2 (bases 1 to 1734)
AUTHORS An.S.
TITLE Direct Submission
JOURNAL Submitted (28-JUN-1997) Medicine, UCSF, 533 Parnassus Ave., Rm U08, San Francisco, CA 94143-0711, USA
FEATURES Location/Qualifiers
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BASE COUNT 302 a 543 c 506 g 383 t

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DEFINITION  Homo sapiens G protein-coupled receptor Edg-4 mRNA, complete cds.
ACCESSION   AF011466
VERSION     AF011466.1
KEYWORDS    GI:2735848
SOURCE      human.
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1734)
AUTHORS    An.S., Bled, R., Hallmark, O.G. and Goetzl, E.J.
TITLE      Characterization of a novel subtype of human G protein-coupled
           receptor for lysophosphatidic acid
JOURNAL     J. Biol. Chem. 273 (14), 7906-7910 (1998)
MEDLINE     98192573
REFERENCE   2 (bases 1 to 1734)
AUTHORS    An.S.
TITLE      Direct Submission
JOURNAL     Submitted (28-JUN-1997) Medicine, UCSF, 533 Parnassus Ave., Rm Ub8,
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FEATURES             Location/Qualifiers
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gb_ro:AY011706      + 798.50 1142.41 2.3e-55 978 ! AY011706 Mus musculus EDG1 (
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seq_name: gb_pr:AF034780

seq_documentation_block:

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LOCUS       AF034780      1062 bp      mRNA                      PRI      01-JAN-1999
DEFINITION  Homo sapiens lysosphingolipid receptor Edg5 mRNA; complete cds.
ACCESSION   AF034780
VERSION     AF034780.1  GI:4090955
KEYWORDS
SOURCE      human.
ORGANISM    Homo sapiens
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1062)
AUTHORS     MacLennan,A.J., Browe,C.S., Gaskin,A.A., Lado,D.C. and Shaw,G.
TITLE       Cloning and characterization of a putative G-protein coupled
             receptor potentially involved in development
JOURNAL     Mol. Cell. Neurosci. 5 (3), 201-209 (1994)
MEDLINE     94373324
REFERENCE   2 (bases 1 to 1062)
AUTHORS     An,S.
TITLE       Edg5, a Human homolog of rat H218 that is a functional receptor for
             lysosphingolipids
JOURNAL     Unpublished
REFERENCE   3 (bases 1 to 1062)
AUTHORS     An,S.
TITLE       Direct Submission
JOURNAL     Submitted (16-NOV-1997) Medicine, UC-San Francisco, 533 Parnassus
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                             VLGGPLILGWNCILGHLEACSTVLPLYAKHYVLCVVTIFSIIILLAIVALYVRIYCVVRS
                             SHADMAAPQTLALLKTVTVLGVFIVCWLPAFSILLDDYACPVHSCPILYKAHYFFAV
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BASE COUNT   166 a   367 c   294 g   235 t
ORIGIN

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alignment_scores:

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Quality: 1780.00      Length: 353
Ratio: 5.086          Gaps: 0
Percent Similarity: 99.150  Percent Identity: 99.150

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alignment_block:

US-09-274-752D-3 x AF034780

Align seg 1/1 to: AF034780 from: 1 to: 1062

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1 MetGlySerLeuTyrSerGluTyrLeuAsnProAsnLysValGlnGluHi 17
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1 ATGGGCAGCTTGTAAGTACGAGTACCTGAACCCCAACAAGTCCAGGAACA 50

17 sTyrAsnTyrThrLysGluThrLeuGluThrGlnGluThrThrSerArgG 34
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51 CTATAATTATACCAAGGAGACGCTGGAACGACGAGAGACGACCTCCCGCC 100

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34 lnValAlaSerAlaGlyIleValIleLeuCysCysAlaIleValValGlu 50
|||||
101 AGTGGCCCTCGGCCCTTCATCGTCATCTCTGTGGCCATTGTGGTGA 150
51 AsnLeuLeuValLeuIleAlaValAlaArgAsnSerLysPheHisSerAl 67
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151 AACCTTCTGGTGTCTATTGCGGTGGCCGAAACAGCAAGTTCACACTCGGC 200
67 aMetTyrLeuPheLeuGlyAsnLeuAlaAlaSerAspLeuLeuAlaGly 84
|||||
201 AATGTACCTGTTCTGGCAACCTGGCCGCTCCGATCTACTGGCAGGCG 250
84 alAlaPheValAlaAsnThrLeuLeuSerGlySerValThrLeuArgLeu 100
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101 ThrProValGlnTrpPheAlaArgGluGlySerAlaSerIleThrLeuSe 117
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134 leAlaLysValLysLeuTyrGlySerCysLysSerCysArgMetLeuLeu 150
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151 LeuIleGlyAlaSerTrpLeuIleSerLeuValLeuGlyLeuProI 167
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167 eLeuGlyTrpAsnCysLeuGlyHisLeuGluAlaCysSerThrValLeu 184
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601 ATCTGTGTGGCCATCGTGGCCCTGTAGTGGCATCTACTGCTGCTGCTCG 650
217 gSerSerHisAlaAspMetAlaAlaProGlnThrLeuAlaLeuLysT 234
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651 CTCAGCCACGCTGACATGGCCGCCCGCCAGACGCTAGCCCTGCTCAAGA 700
234 hrValThrIleValLeuGlyValPheIleValCysTrpLeuProAlaPhe 250
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301 ArgProLeuGlnCysTrpArgProGlyValGlyValGlnGlyArgArg 317
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901 CGGCCCTGCAAGTGTGGCGCGGGGGTGGGGTGCAGGAGGAGGCG 950
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951 GGTGGGACCCCGGGCCACACCTCTGTCCACTCCGACGCTCCAGCTCC 1000

334 euGluArgGlyMethHisMetProThrSerProThrPheLeuGluGlyAsn 350
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1001 TGGAGAGGGGCATGCACATGCCACGTCACCCACGTTTCTGGAGGGCAAC 1050
351 ThrValVal 353
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1051 ACGGTGGTC 1059

ALIGNMENTS

RESULT 1
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 LOCUS AF034780 1062 bp mRNA PRI 01-JAN-1999
 DEFINITION Homo sapiens lysosphingolipid receptor Edg5 mRNA, complete cds.
 ACCESSION AF034780
 VERSION AF034780.1 GI:4090955
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1062)
 AUTHORS MacLennan, A.J., Browe, C.S., Gaskin, A.A., Lado, D.C. and Shaw, G.
 TITLE Cloning and characterization of a putative G-protein coupled
 receptor potentially involved in development
 JOURNAL Mol. Cell. Neurosci. 5 (3), 201-209 (1994)
 MEDLINE 94373324
 REFERENCE 2 (bases 1 to 1062)
 AUTHORS An, S.
 TITLE Edg5, a Human homolog of rat H218 that is a functional receptor for

